

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 23:26:15 ; Search time 7703 Seconds  
(without alignments)  
10939.950 Million cell updates/sec

Title: US-10-765-580-11  
Perfect score: 1507  
Sequence: 1 atgacacatcatcatcatca.....gtgacaaagccagcgctga 1507

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues  
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: gb\_est1.\*  
2: gb\_est3.\*  
3: gb\_est4.\*  
4: gb\_est5.\*  
5: gb\_est6.\*  
6: gb\_est7.\*  
7: gb\_est8.\*  
8: gb\_est9.\*  
9: gb\_est10.\*  
10: gb\_est11.\*  
11: gb\_est12.\*  
12: gb\_est13.\*  
13: gb\_est14.\*  
14: gb\_est15.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	33.0	510	AY407604	AY407604 Homo sapi
2	484.6	32.2	988	BX442364	BX442364 BX442364
3	484.4	32.1	3562	BC058855	BC058855 Homo sapi
4	421.8	28.0	520	DN350259	DN350259 LIBS579-0
5	400	26.5	510	AY407605	AY407605 Pan trogl
6	370.2	24.6	828	CO886262	CO886262 Boygen_14
7	363.6	24.1	485	AY407606	AY407606 Mus muscu
8	344	22.8	535	DB278789	DB278789 DB278789
9	344	22.8	547	AU279816	AU279816 AU279816
10	327.2	21.7	791	CK364171	CK364171 AGENCOURT
11	326.8	21.4	528	BO674897	BO674897 603393614
12	323.2	21.4	890	BI869727	BI869727 6023-75 M
13	323.2	21.4	600	BU919454	BU919454 6023-75 M
14	322.2	20.8	1683	CR614384	CR614384 full-length
15	314	20.7	459	AI591060	AI591060 tw28f02.x
16	312.4	19.6	752	CA505431	CA505431 UI-R-FSI-
17	296	19.3	953	BO713895	BO713895 AGENCOURT
18	291.4	18.9	904	BX426783	BX426783 BX426783
19	285	18.9	904	BX426783	BX426783 BX426783

20	276	18.3	558	9	DA172761
21	268	17.8	799	5 <td>CK465017</td>	CK465017
22	261.6	17.4	752	3 <td>BO780197</td>	BO780197
23	261	17.3	613	3 <td>BO832724</td>	BO832724
24	261	17.3	803	9 <td>CK898524</td>	CK898524
25	260	17.3	490	4 <td>CB725648</td>	CB725648
26	254.4	16.9	726	8 <td>CK009700</td>	CK009700
27	249.8	16.6	495	4 <td>BX445267</td>	BX445267
28	248.8	16.5	543	2 <td>BG311141</td>	BG311141
29	241	16.0	632	5 <td>CK479447</td>	CK479447
30	235.4	15.6	920	3 <td>BU848858</td>	BU848858
31	234.8	15.6	777	5 <td>CK367183</td>	CK367183
32	227.8	15.5	533	7 <td>BF514775</td>	BF514775
33	227.8	15.1	600	3 <td>BQ208280</td>	BQ208280
34	227.6	15.1	924	3 <td>BU153227</td>	BU153227
35	225.8	15.0	887	3 <td>BQ959864</td>	BQ959864
36	223.6	14.8	689	3 <td>BQ199378</td>	BQ199378
37	222.2	14.7	601	8 <td>CK234175</td>	CK234175
38	217.2	14.4	639	10 <td>DT887832</td>	DT887832
39	217	14.4	442	7 <td>AM118848</td>	AM118848
40	214	14.2	301	7 <td>BE166543</td>	BE166543
41	207.2	13.7	600	2 <td>BG803325</td>	BG803325
42	204	13.5	534	3 <td>BM991154</td>	BM991154
43	203.2	13.2	649	7 <td>BF679862</td>	BF679862
44	199.6	12.9	244	2 <td>BF841362</td>	BF841362
45	195	12.9	521	7 <td>AM630808</td>	AM630808

## ALIGNMENTS

RESULT 1  
AY407604  
LOCUS  
DEFINITION Homo sapiens VEGF gene, VIRTUAL TRANSCRIPT, partial sequence.  
ACCESSION AY407604  
VERSION AY407604.1  
KEYWORDS GSS.  
ORGANISM Homo sapiens (human)  
SOURCE  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Snitsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

1 (bases 1 to 510)  
2 (bases 1 to 510)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Snitsky,J.J.,  
Adams,M.D. and Cargill,M.

Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
source

1. 510  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
1..>510  
/gene="VEGF"  
/locus\_tag="HCCN2946"

ORIGIN



Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loggiano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McEwan, K.J., Malek, U.A., Gunaratne, P.H., Richards, S., Wooley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, X., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.B., Schnerch, A., Schein, J.E., Jones, S.J., Skalska, U., and Marra, M.A.

Mammalian Gene Collection Program Team  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932  
2 (bases 1 to 3562)

NIH MGC Project  
Direct Submission  
Submitted (01-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegod, H., Kovits, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nananavali, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 91 Row: n Column: 1  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 71051577  
This clone has the following problem: frame shifted.

## FEATURES

## SOURCE

1. 3562  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5313912"  
/tissue\_type="Brain, hypothalamus"  
/clone\_lib="NIH\_MGC\_96"  
/lab\_host="DH10B"  
/note="Vector: pBluescript"

## ORIGIN

Query Match 32.1%; Score 484.4; DB 6; Length 3562;  
Best Local Similarity 99.6%; Pred. No. 4.8e-134;  
Matches 496; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1010 GCACCCATGCGAGAGAGAGGCGAGATCATCGAAGTGGTGAAGTTCTGATGTC 1069  
DB 1114 GCACCATGCGAGAGAGAGGCGAGATCATCGAAGTGGTGAAGTTCTGATGTC 1173  
QY 1070 TATCAGCGAGTATCGCATCAATCGAGACCTGGTGGAGATCTTCCAGAGTACCT 1129  
DB 1174 TATCAGCGAGTATCGCATCAATCGAGACCTGGTGGAGATCTTCCAGAGTACCT 1233  
QY 1130 GATGAGTGCATCATCTTCAAGCATCTGTGGCCCTGATGAGTGCAGGAGGCTGC 1189

DB 1234 GATGAGTGCATCATCTTCAAGCATCTGTGGCCCTGATGAGTGCAGGAGGCTGC 1293  
QY 1190 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGATCCAAATCAACATGAGATT 1249  
DB 1294 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGATCCAAATCAACATGAGATT 1353  
QY 1250 ATGCGGATCAAACTTCACCAAGGCGACATATGAGATGAGTCTTCTACAGCAAC 1309  
DB 1354 ATGCGGATCAAACTTCACCAAGGCGACATATGAGATGAGTCTTCTACAGCAAC 1413  
QY 1310 AATGTGAATGACAGCAAAAGATAGACAGCAAGAAATCTCTGTGGCTTGC 1369  
DB 1414 AATGTGAATGACAGCAAAAGATAGACAGCAAGAAATCTCTGTGGCTTGC 1473  
QY 1370 TCAGAGCGGAGAAAGATTTTGTGACAGATCCGCAACCTGTAAATGTCCTGCAA 1429  
DB 1474 TCAGAGCGGAGAAAGATTTTGTGACAGATCCGCAACCTGTAAATGTCCTGCAA 1532  
QY 1430 AACAGACTCGGCTTGAAGGCGAGGAGCTTGAAGTAAACGAGTACTGACATGT 1489  
DB 1533 AACAGACTCGGCTTGAAGGCGAGGAGCTTGAAGTAAACGAGTACTGACATGT 1592  
QY 1490 GACAAGCCGAGGCGGTGA 1507  
DB 1593 GACAAGCCGAGGCGGTGA 1610

RESULT 4  
DN350259 520 bp mRNA linear EST 04-MAR-2005  
LOCUS LIB3579-026-Q1-K1-H10 LIB3579 Canis familiaris cDNA clone  
DEFINITION CAN2484766, mRNA sequence.  
ACCESSION DN350259  
VERSION DN350259.1 GI:60522951  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 520)  
AUTHORS Staten, N.R.  
TITLE Direct Submission (Staten, N.R.)  
JOURNAL Unpublished (2005)  
COMMENT Contact: Nick Staten  
Tel: 636 247 6855  
Email: [nicholas.r.staten@pfizer.com](mailto:nicholas.r.staten@pfizer.com).

## FEATURES

## SOURCE

1. 520  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/strain="Beagle"  
/db\_xref="taxon:9615"  
/clone="CAN2484766"  
/tissue\_type="thyroid"  
/lab\_host="DH10B"  
/clone\_lib="LIB3579"  
/note="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; control dog"

## ORIGIN

Query Match 28.0%; Score 421.8; DB 9; Length 520;  
Best Local Similarity 92.3%; Pred. No. 2e-115;  
Matches 444; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1006 CAAGGACCCATGCGAGAGAGAGGCGAGATCATCGAAGTGGTGAAGTTCTATGCA 1065  
DB 40 CAAGGCTCGGCTATGCGAGAGAGAGGCGAGATCATCGAAGTGGTGAAGTTCTATGCA 99  
QY 1066 TGTCTATAGGCGAGCTACTGCCATCAATCGAGACCTGTGGAGATCTTCCAGAGTA 1125  
DB 100 CGTTCACGAGCGAGACTACTGCCATCAATCGAGACCTGTGGAGATCTTCCAGAGTA 159

QY 1126 CCTGATGAGATGAGTACATCTTCAAGCCATCTGTGTGCCCCCTGATGCGAGG 1185  
 DB 160 CCTGACGAGATGAGTACATCTTCAAGCCATCTGTGTGCCCCCTGATGCGAGG 219  
 QY 1186 CTGCTGATGAGTACGAGGCTGTGAGTGTGCCCCCTGAGAGTCCATCATCCATCA 1245  
 DB 220 CTGCTGATGAGTACGAGGCTGTGAGTGTGCCCCCTGAGAGTCCATCATCCATCA 279  
 QY 1246 GATTATGCGGATCAAACTCACCAGAGCCAGACATAGAGAGATGAGCTTCTACACA 1305  
 DB 280 GATTATGCGGATCAAACTCACCAGAGCCAGACATAGAGAGATGAGCTTCTACACA 339  
 QY 1306 CAACAATGTGAATGAGACCAAGAAAGATAGAGACAGAAATCCCTGTGGGCC 1365  
 DB 340 TACCAATGTGAATGAGACCAAGAAAGATAGAGACAGAAATCCCTGTGGGCC 399  
 QY 1366 TTGCTGAGAGCGGAGAAAGCATTTTGTGTACAAAGTCCGAGAGTGAATGTCTCG 1425  
 DB 400 TTGCTGAGAGCGGAGAAAGCATTTTGTGTACAAAGTCCGAGAGTGAATGTCTCG 459  
 QY 1426 CAAAAACAGACTCCGCTTGCAAGCGGAGAGCTTGATTAAAGAACTACTTGCGAG 1485  
 DB 460 CAAAAACAGACTCCGCTTGCAAGCGGAGAGCTTGATTAAAGAACTACTTGCGAG 519  
 QY 1486 A 1486  
 DB 520 A 520

RESULT 5  
 AY407605 510 bp DNA linear GSS 15-DEC-2003  
 LOCUS Pan troglodytes VEGF gene, VIRUAL TRANSCRIPT, partial sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AY407605  
 VERSION AY407605.1 GI:39763576  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Pan  
 1 (bases 1 to 510)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civejlo, D.R., Lu, F., Murphy, B.,  
 Perrier, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 Science 302 (5652), 1960-1963 (2003)  
 JOURNAL  
 PUBMED 14671302  
 2 (bases 1 to 510)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civejlo, D.R., Lu, F., Murphy, B.,  
 Perrier, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment  
 FEATURES  
 Location/Qualifiers  
 source  
 1..510  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 <1..>510  
 /gene="VEGF"  
 /locus\_tag="HCM2946"

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 Best Local Similarity 80.3%; Pred. No. 7.9e-109;

Matches 400; Conservative 0; Mismatches 98; Indels 0; Gaps 0;  
 QY 1010 GCACCCATGCGAAGAGAGAGGAGAGATCATCATCAATGTGTGAATCATGAGATGC 1069  
 DB 13 GCACCCATGCGAAGAGAGAGGAGAGATCATCATCAATGTGTGAATCATGAGATGC 72  
 QY 1070 TATCAGGCGAGTCTGTCGATCCATCCAGAGACCCTGTGTGACATCTTCCAGAGTACCT 1129  
 DB 73 TATCAGGCGAGTCTGTCGATCCATCCAGAGACCCTGTGTGACATCTTCCAGAGTACCT 132  
 QY 1130 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCCCTGATGCGAGGCGCTGC 1189  
 DB 133 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCCCTGATGCGAGGCGCTGC 192  
 QY 1190 TGCATGACGAGGCGCTGTGAGTGTGTGCCCCCTGATGAGAGTCCATCATCCATGAGATT 1249  
 DB 193 TGCATGACGAGGCGCTGTGAGTGTGTGCCCCCTGATGAGAGTCCATCATCCATGAGATT 252  
 QY 1250 ATGGGAGTCAAACTCACCAGGCGAGACATAGAGAGATGAGCTTCTTACAGACACAC 1309  
 DB 253 ATGGGAGTCAAACTCACCAGGCGAGACATAGAGAGATGAGCTTCTTACAGACACAC 312  
 QY 1310 AAATGTGAATGAGACCAAGAAAGATAGAGACCAAGAAATCCCTGTGGGCCCTTGC 1369  
 DB 313 AAATGTGAATGAGACCAAGAAAGATAGAGACCAAGAAATCCCTGTGGGCCCTTGC 372  
 QY 1370 TCAGAGCGGAGAAAGCATTTTGTGTGTCAAGATCCGAGAGCTTAAATGTCTGTGCAA 1429  
 DB 373 TCAGAGCGGAGAAAGCATTTTGTGTGTCAAGATCCGAGAGCTTAAATGTCTGTGCAA 432  
 QY 1430 AACACAGACTCGCTTGCAAGCGGAGAGCTTGATTAAAGAACTACTTGCGAGATCT 1489  
 DB 433 NNN 492  
 QY 1490 GACAGCCGAGCGGCTGA 1507  
 DB 493 GACAGCCGAGCGGCTGA 510

RESULT 6  
 CO886262 828 bp mRNA linear EST 01-SEP-2004  
 LOCUS Bovgen.14587 normal cattle brain Bos taurus cDNA clone  
 DEFINITION RZPDP1056P0311Q 5', mRNA sequence.  
 ACCESSION CO886262  
 VERSION CO886262.1 GI:51816547  
 KEYWORDS EST.  
 SOURCE Bos taurus (cattle)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 828)  
 Hennig, S., Janitz, M., Herwig, R. and Williams, J.  
 Generation, annotation, evolutionary analysis and database  
 integration of 14969 cattle EST clusters  
 unpublished (2004)  
 JOURNAL  
 CONTACT Hennig S  
 Laboratory 123, dep. Lehrach  
 Max-Planck-Institut fuer Molekulare Genetik  
 Ihnestr.63-73, D-14195 Berlin, Germany  
 Tel: +49 30 8413 1612  
 Fax: +49 30 8413 1380  
 Email: hennig@molgen.mpg.de  
 The library was characterised by oligonucleotide fingerprinting  
 (ONFP) to reduce sequencing redundancy. According to the ONFP  
 procedure, clones that display the same hybridisation matrix with a  
 battery of 200 8mer oligonucleotides are grouped into clusters. One  
 clone per ONFP cluster was selected for sequencing. cDNA clones and  
 filters are distributed via Deutsches Ressourcenzentrum fuer  
 Genomforschung GmbH (http://www.rzpd.de).  
 PCR Primers  
 FORWARD: 5' CCCGAGCTTACACTTATGTTCCGGCTCG 3' (M13RSP) 5'-seq



FEATURES  
source

BACKWARD: 5' GCTATTACGCCAGCTGGCGAAGGGGATG 3' (M13RSP) 3'-seq  
Seq primer: 5'-CCGGTCCGGAATTCCTCCGGGT-3' (M13RSP).  
Location/Qualifiers  
1. 828  
/organism="Bos taurus"  
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/db\_xref="taxon:9913"  
/clone="R2PDP1056P0311Q"  
/sex="female"  
/tissue\_type="brain tissue"  
/dev\_stage="adult brain"  
/clone\_lib="normal cattle brain"  
/note="Organ: brain; Vector: pSPORT1; Site: 1: NotI;  
Site 2: SalI; Random primed and directionally cloned in  
pSPORT1 vector using NotI  
15'-PACCTAGTCTAGATCGGAGCGGCGCC (T)15-3' and SalI 5'-  
TCGACCCACGGCTCCG-3' adapters (Gibco BRL)"

## ORIGIN

Query Match 24.6%; Score 370.2; DB 8; Length 828;  
Best Local Similarity 95.5%; Pred. No. 9.6e-100;  
Matches 381; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

1109 GACATCTTCAGAGATCCCTGATGATGATCGATCATCTTCAACCCATCTCTGTGCCC 1168  
1169 CTGATGCGATGCGGGGGCTGCGAATGACGAGGGCTGAGTGTGTCCTCCACGAGAG 1228  
66 CTGATGCGGATGCGGGGGCTGCGAATGACGAGGGCTGAGTGTGTCCTCCACGAGAG 125  
1229 TCCACATCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1288  
126 TTCAACATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 185  
1289 ATGAGCTTCATGACGACCAATGATGATGATGATGATGATGATGATGATGATGATG 1348  
186 ATGAGCTTCATGACGACCAATGATGATGATGATGATGATGATGATGATGATGATG 245  
1349 GAAATATCCCTGAGGCTGCTCAGAGCGGAGAAAGCATTTGTTGTCAAGATCCGAG 1408  
246 GAAATATCCCTGAGGCTGCTCAGAGCGGAGAAAGCATTTGTTGTCAAGATCCGAG 305  
1409 ACGTGTAAATGTTCTGCAAAAACACAGCTGCGTTGCAAGCGCAGCTTGAATTA 1468  
306 ACGTGTAAATGTTCTGCAAAAACACAGCTGCGTTGCAAGCGCAGCTTGAATTA 365  
1469 AACGAACGATCTTGCAGATGATGACCAAGCGGAGCGGCTGA 1507  
366 AACGAACGATCTTGCAGATGATGACCAAGCGGAGCGGCTGA 404

RESULT 7  
LOCUS AY407606 485 bp DNA linear GSS 15-DEC-2003  
DEFINITION Mus musculus VEGF gene, VIRUTAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY407606  
VERSION AY407606.1 GI:39763577  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Slnsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302  
REFERENCE 2 (bases 1 to 485)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Slnsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
source  
Location/Qualifiers  
1. 485  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/gene="VEGF"  
/locus\_tag="HGM2946"

## ORIGIN

Query Match 24.1%; Score 363.6; DB 14; Length 485;  
Best Local Similarity 82.5%; Pred. No. 7.9e-98;  
Matches 396; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

1006 CAAGGACCCATGCGCAG 1065  
6 CCAGCTGACACCCAGCAG 65  
1066 TGTCTATCAGCGAGCTACTCCATCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1125  
66 TGTCTATCAGCGAGAGCTACTCCATCCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 125  
1126 CCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1185  
126 CCCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 185  
1186 CTGCTGCAATGACGAGGCTGAGAGTGTGTCCTCCACGAGAGTCCATCACCATGCA 1245  
186 CTGCTGCAATGACGAGGCTGAGAGTGTGTCCTCCACGAGAGTCCATCACCATGCA 245  
1246 GATTATGCGGATCAAACTCTACCAAGGCTCAGACATAGAGAGATGAGCTTCTACACA 1305  
246 GATTATGCGGATCAAACTCTACCAAGGCTCAGACATAGAGAGATGAGCTTCTACACA 305  
1306 CAACAAATGTGATCCAGACCAAGAGAAAGATAGACCAAGAAATCCCTGTGGGCC 1365  
306 CAGCAGATGTGAATGACAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 365  
1366 TTGCTCAGAGCGGAGAAAGCATTTGTTGTCAAGATCCGAGAGCTGTAATGTTCTG 1425  
366 TTGCTCAGAGCGGAGAAAGCATTTGTTGTCAAGATCCGAGAGCTGTAATGTTCTG 425  
1426 CAAAAACAGAGCTGCGCTTGCAGCGAGCGAGCTTGAAGTTAAAGAAAGTACTTGCAG 1485  
426 CAAAAACAGAGCTGCGCTTGCAGCGAGCGAGCTTGAAGTTAAAGAAAGTACTTGCAG 485

RESULT 8  
LOCUS DB278789 535 bp mRNA linear EST 10-DEC-2005  
DEFINITION DB278789 UTERU3 Homo sapiens cDNA clone UTERU3004919 5', mRNA  
sequence.  
ACCESSION DB278789  
VERSION DB278789.1 GI:83443806  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Oca,T., Nishikawa,T.,

## TITLE

JOURNAL  
PUBMED  
COMMENT

Yamauchi, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Iishi, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kishida, N., Yonekawa, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Magatsuma, M., Morikawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification and Characterization of Putative Alternative Promoters of Human Genes  
Genome Res. 16 (1), 55-65 (2006)  
16344560  
Contact: Takao Isogai  
FLJ Project (HRI Team)  
Helix Research Institute  
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: flj-cdna@nifty.com  
NEDO human CDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB  
Location/Qualifiers

FEATURES  
source  
1. .535  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/note="Vector: PME18SFL3"

## ORIGIN

Query Match 22.8%; Score 344; DB 9; Length 535;  
Best Local Similarity 100.0%; Pred. No. 6.8e-92; Indels 0; Gaps 0;  
Matches 344; Conservative 0; Mismatches 0;

QY 1010 GCACCCATGGCAGAGAGAGAGAGAGAGAGATCATCAGAGTGTGAAATTCATGATGTC 1069  
DB 173 GCACCCATGGCAGAGAGAGAGAGAGAGATCATCAGAGTGTGAAATTCATGATGTC 232  
QY 1070 TATACAGCAGACTACTGCCATCCATGAGACCTGTGTGACATCTTCAGAGTACCT 1129  
DB 233 TATACAGCAGACTACTGCCATCCATGAGACCTGTGTGACATCTTCAGAGTACCT 232  
QY 1130 GATGAGATCGAGTACTCTTCAAGCCATCTGTGTGCTGATGCGATCGGGGCTGC 1189  
DB 293 GATGAGATCGAGTACTCTTCAAGCCATCTGTGTGCTGATGCGATCGGGGCTGC 352  
QY 1190 TGCATGACGAGGCTGTGAGTGTGCTGCTGAGAGTCCAAATCATTACATGATG 1249  
DB 353 TGCATGACGAGGCTGTGAGTGTGCTGCTGAGAGTCCAAATCATTACATGATG 412  
QY 1250 ATGGGATCAAACTCTCAAGGCGCAGACATAGAGAGTACCTTCTTACACACAC 1309  
DB 413 ATGGGATCAAACTCTCAAGGCGCAGACATAGAGAGTACCTTCTTACACACAC 472  
QY 1310 AAATGTGATGACAGACCAAGAAAGATAGACAGACAGAAAA 1353  
DB 473 AAATGTGATGACAGACCAAGAAAGATAGACAGACAGAAAA 516

RESULT 9  
AU279816 547 bp mRNA linear EST 31-JUL-2003  
LOCUS AU279816 CHONS2 Homo sapiens cDNA clone CHONS2001577 5', mRNA  
DEFINITION sequence.  
ACCESSION AU279816  
VERSION AU279816.1 GI:28299043  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
COMMENT

Imabayashi, H., Mori, T., Gojo, S., Kiyono, T., Sugiyama, T., Irie, R., Isogai, T., Hata, J., Tomoya, Y. and Umezawa, A. Redifferentiation of dedifferentiated chondrocytes and chondrogenesis of human bone marrow stromal cells via chondrosphere formation with expression profiling by large-scale cDNA analysis  
Exp. Cell Res. 288 (1), 35-50 (2003)  
12878157

Contact: Takao Isogai  
FLJ Project (HRI Team)  
Helix Research Institute  
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: flj-cdna@nifty.com  
HRI human CDNA Project, Sugiyama, T.; Wakamatsu, A.; Irie, R.; Umezawa, A.; Fukuma, M.; Kusakari, S.; Hata, J.; Iishi, S.; Yamamoto, J.; Isono, Y.; Saito, K.; Nakamura, Y.; Masuno, Y.; Nagai, K.; Isogai, T. HRI human CDNA project; cDNA library construction & 5'-end one pass sequencing: Helix Research Institute.  
Location/Qualifiers

FEATURES  
source  
1. .547  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CHONS2001577"  
/cell\_type="chondrocytes"  
/clone\_id="CHONS2"  
/note="Vector: PME18SFL3"

## ORIGIN

Query Match 22.8%; Score 344; DB 1; Length 547;  
Best Local Similarity 100.0%; Pred. No. 6.9e-92; Indels 0; Gaps 0;  
Matches 344; Conservative 0; Mismatches 0;

QY 1010 GCACCCATGGCAGAGAGAGAGAGAGAGATCATCAGAGTGTGAAATTCATGATGTC 1069  
DB 6 GCACCCATGGCAGAGAGAGAGAGAGAGATCATCAGAGTGTGAAATTCATGATGTC 65  
QY 1070 TATACAGCAGACTACTGCCATCCATGAGACCTGTGTGACATCTTCAGAGTACCT 1129  
DB 66 TATACAGCAGACTACTGCCATCCATGAGACCTGTGTGACATCTTCAGAGTACCT 125  
QY 1130 GATGAGATCGAGTACTCTTCAAGCCATCTGTGTGCTGATGCGATCGGGGCTGC 1189  
DB 126 GATGAGATCGAGTACTCTTCAAGCCATCTGTGTGCTGATGCGATCGGGGCTGC 185  
QY 1190 TGCATGACGAGGCTGTGAGTGTGCTGCTGAGAGTCCAAATCATTACATGATG 1249  
DB 186 TGCATGACGAGGCTGTGAGTGTGCTGCTGAGAGTCCAAATCATTACATGATG 245  
QY 1250 ATGGGATCAAACTCTCAAGGCGCAGACATAGAGAGTACCTTCTTACACACAC 1309  
DB 246 ATGGGATCAAACTCTCAAGGCGCAGACATAGAGAGTACCTTCTTACACACAC 305  
QY 1310 AAATGTGATGACAGACCAAGAAAGATAGACAGACAGAAAA 1353  
DB 306 AAATGTGATGACAGACCAAGAAAGATAGACAGACAGAAAA 349

RESULT 10  
BX443079 880 bp mRNA linear EST 04-MAY-2004  
LOCUS BX443079 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA  
DEFINITION clone CS0D0004YG03 5-PRIME, mRNA sequence.  
ACCESSION BX443079  
VERSION BX443079.2 GI:47001997  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens



QY 1354 -----TC 1355  
 Db 361 GAAAGGAAAGGGTCAAAAAGCAAGCCGCAAGAAATCCGGTTAAATCTGAGCGCTC 420  
 QY 1356 CCTGTGGGCTTGTCTCAGAGCGGAGAAAGCATTTTGTTCACAGATCCGAGCGTGA 1415  
 Db 421 ACTGTAGCCTTGTCTCAGAGCGGAGAAAGCATTTTGTTCACAGATCCGAGCGTGA 480  
 QY 1416 AATGTTCTGCAAAAACACAGACTGCGCTTGCAAGCGGAGCGAGCTTGAATTAACGAC 1475  
 Db 481 AATGTTCTGCAAAAACACAGACTGCGCTTGCAAGCGGAGCGAGCTTGAATTAACGAC 540  
 QY 1476 GTACTTGACAGATGTGACAGCCGAGCGGCTGA 1507  
 Db 541 GTACTTGACAGATGTGACAGCCGAGCGGCTGA 572  
 RESULT 12  
 B0674897 528 bp mRNA linear EST 15-JUL-2002  
 LOCUS B0674897  
 DEFINITION AGENCOURT 8036450 NIH\_MGC\_102 Homo sapiens CDNA clone IMAGE:6212223  
 5' mRNA sequence.  
 ACCESSION B0674897  
 VERSION B0674897.1 GI:21785731  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 528)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LCM2375 row: p column: 16  
 High quality sequence stop: 527.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6212223"  
 /tissue\_type="epidermoid carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1lb="NIH MGC 102"  
 /note="Organ: salivary gland; Vector: pOT7; Site\_1: XhoI;  
 Site\_2: EcoRI; CDNA made by oligo-dt priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAAGAG(G). Library constructed  
 by Ling Hong in the laboratory of Gerald M. Rubin  
 (University of California, Berkeley) using ZAP-CDNA  
 synthesis kit (Stratagene) and Superscript II RT (Life  
 Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 21.4%; Score 323.2; DB 3; Length 528;  
 Best Local Similarity 96.2%; Pred. No. 1.3e-85;  
 Matches 331; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1010 GCACCCATGCGAGAGAGAGGCGCAGATCATCAGAGAGTGTGAAGTTTCATGATGTC 1069  
 Db 174 GCACCCATGCGAGAGAGAGGCGCAGATCATCAGAGAGTGTGAAGTTTCATGATGTC 233

QY 1070 TATCAGGCGAGCTACTGCTCCATTCATGAGAGCCCTGGTGAATCTTCCAGAGTACCT 1129  
 Db 234 TATCAGGCGAGCTACTGCTCCATTCATGAGAGCCCTGGTGAATCTTCCAGAGTACCT 293  
 QY 1130 GATGAGATCAGTACATCTTTCAGACCATCTGTGTGCTCCCTGATTCGATTCGGGGCTGC 1189  
 Db 294 GATGAGATCAGTACATCTTTCAGACCATCTGTGTGCTCCCTGATTCGATTCGGGGCTGC 353  
 QY 1190 TGCATATCAGAGGCGCTGAGATGTGTCGCCACTGAGAGATCCAAATCACCATGAGATT 1249  
 Db 354 TGCATATCAGAGGCGCTGAGATGTGTCGCCACTGAGAGATCCAAATCACCATGAGATT 413  
 QY 1250 ATGCGATCAAACTCTCAAGGCGAGCAGATGAGAGATGAGCTTCTTACAGACAC 1309  
 Db 414 ATGCGATCAAACTCTCAAGGCGAGCAGCAGATGAGAGATGAGCTTCTTACAGACAC 473  
 QY 1310 AATATGATGACAGACCAAGAAAGATGAGCAAGACAGAGAA 1353  
 Db 474 AATATGATGACAGACCAAGAAAGATGAGCAAGAGAGAA 517

RESULT 13  
 B1869727 890 bp mRNA linear EST 11-OCT-2001  
 LOCUS B1869727  
 DEFINITION 603393614P1 NIH\_MGC\_90 Homo sapiens CDNA clone IMAGE:5403771 5',  
 mRNA sequence.  
 ACCESSION B1869727  
 VERSION B1869727.1 GI:16043400  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 890)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM12029 row: k column: 04  
 High quality sequence stop: 733.  
 Location/Qualifiers  
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 /clone\_1lb="NIH MGC 90"  
 /note="Organ: liver; Vector: pCMV-Sport6; Site\_1: NotI;  
 Site\_2: SalI; cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.7 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## FEATURES

source  
 1..890  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5403771"  
 /tissue\_type="adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1lb="NIH MGC 90"  
 /note="Organ: liver; Vector: pCMV-Sport6; Site\_1: NotI;  
 Site\_2: SalI; cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.7 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 21.4%; Score 323.2; DB 2; Length 890;  
 Best Local Similarity 99.1%; Pred. No. 1.6e-85;  
 Matches 325; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1058 TTTCATGATGTCATATCAGGCGAGCTACTGCGATTCATCAGAGCCCTGTGTGACATCTTC 1117  
 Db 1 TTTCATGATGTCATATCAGGCGAGCTACTGCGATTCATCAGAGCCCTGTGTGACATCTTC 60

Qy	1118	TAGGAGTACCCGTAATGAGATGAGTAATCTTTCAAGGCATCTGTGTGCCCTGATCGA	1177
Db	61	CAGAGATACCCGTGATGAGATGAGTACATCTTTCAAGGCATCTGTGTGCCCTGATCGA	120
Qy	1178	TGCGGGGGCTGCTGCATGATGACGAGGGCGCTGAGTGTGTGCCCTGAGAGTCCAAATC	1237
Db	121	TGCGGGGGCTGCTGCATGATGAGAGGGCGCTGAGTGTGTGCCCTGAGAGTCCAAATC	180
Qy	1238	ACCATGTCAGATTTATGCGGATCAAACTTCACCAAGCGCGACATATGAGAGATGAGCTTC	1297
Db	181	ACCATGTCAGATTTATGCGGATCAAACTTCACCAAGCGCGACATATGAGAGATGAGCTTC	240
Qy	1298	CTACAGCACAACAAATGTGAATGCGACGCAAAAGAAAGATAGAGCAAGCAAGAAATTC	1357
Db	241	CTACAGCACAACAAATGTGAATGCGACGCAAAAGAAAGATAGAGCAAGCAAGAAATTC	300
Qy	1358	TGTGGGCGCTTGCTGACGAGCGGAGAAAGC	1385
Db	301	TGTGGGCGCTTGCTGACGAGCGGAGTCCGC	328

RESULT 14	BU919454	LOCUS	DEFINITION
	BU919454	600 bp	mRNA linear EST 30-OCT-2002
	6023-75	Mouse	E14.5 retina lambda ZAP II Library Mus musculus cDNA,
		mRNA sequence.	

ACCESSION	BU919454	
VERSION	BU919454.1	GI:24423290
KEYWORDS	EST.	
SOURCE	Mus musculus	(house mouse)
ORGANISM	Mus musculus	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1. (bases 1 to 600)  
Eubaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
Mi, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scappa, A., Wang, S.W., White, R.A., Belamand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.  
Gene expression in the developing mouse retina by EST sequencing and microarray analysis  
Nucleic Acids Res. 29 (24) 4983-4993 (2001)

**JOURNAL**      **Nucleic Acids Res.**    **29 (24), 4983-4993 (2001)**  
**PUBMED**      **11812828**  
**COMMENT**      **Contact: Klein WH**  
                    **Department of Biochemistry and Molecular Biology**  
                    **University of Texas M.D. Anderson Cancer Center**  
                    **Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA**  
                    **Tel: 713 792 3646**  
                    **Fax: 713 790 0329**

FEATURES	Location/Qualifiers
source	1. .600

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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
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clone_11b="Mouse E14.5 retina lambda ZAP II library"

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ORIGIN

Query Match	Score	DB 3;	Length
21.48;	322.2;	600;	

Best Local Similarity	91.4%	Pred. NO. 2.08e-85			
Matches	342	Conservative	0	Mismatches	33
				Indels	0
				Gaps	0

Qy 1133 GAGATCGGTACATCTTCAAGCCACCTGTGTGCCCCCTGATGCGATGCGGGGCGTGC 1137  
 Db 2 GAGATAGATACATCTTCAAGCCGCTGTGTGCCCCCTGATGCGGCTGTGCAAGCTGCTGT 61

1193 ATGACGAGGCGCTGGAGTGTGTGCCACTGAGAGTCCACATCACCATGCGATTATG 1252

Db 62 AACGATGAAGCCCTGGAGTGCCTGCCACCGTCAGAGAGCAACATCACCATGCGAGATCA19 121

Db 122 CGGATCAAACTTCACCAAGCAGACATAGGAGAGATGAGCTTCCTACAGACACAGAGA 181

Accession	Sequence	Position
OY	1313 TGTGATATGCAGACCAAGAAAGATATAGCAAGACAAAGAAATCCCTGTGGCCCTTGCTCA	1372
Db	182 TGTGAATGCGAGATCCAAAGAAAGACAGACAAAGCCAGAAATCACTGTGACCTTGTTCA	241
OY	1373 GAGCGAGAAAGCATTTGTTGTATCAAGATCCGACAGCTGTAAATGTTCTGCAAAAC	1432
Db	242 GAGCGAGAAAGCATTTGTTGTATCAAGATCCGACAGCTGTAAATGTTCTGCAAAAC	301
OY	1433 ACAGACTCCGCTTGCAAGCGGACGACCTGATTAACGAAGCTTGCAGATGTGAC	1492
Db	302 ACACACTCCGCTTGCAAGCGGACGACCTGATTAACGAAGCTTGCAGATGTGAC	361
OY	1493 AAGCGAGGCGGTGA	1507
Db	362 AAGCCAAAGCGGTGA	376

RESULT 15	
CR614384	
LOCUS	CR614384
DEFINITION	1683 bp mRNA linear HTC 21-JUL-2004
	full-length cDNA clone CSDDM0051514 of Fetal liver of Homo sapiens

ACCESSION	{human} .
VERSION	CR614384
KEYWORDS	CR614384.1 GI:50495191
SOURCE	HTC; CNSLT cDNA.
ORGANISM	Homo sapiens (human)
	Homo sapiens

**ORGANISM** Homo sapiens; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 1683)  
**REFERENCE** Li, W.B., Gruber, C., Jesse, J., and Polyes, D. Full-length cDNA libraries and normalization  
**AUTHORS** unpublished  
**TITLE** Contact : Feng Liang Email : [fliang@lifeitech.com](mailto:fliang@lifeitech.com) URL : <http://www.lifeitech.com> Corporation 1600  
**JOURNAL**  
**REMARK**

REFERENCE  
2 (bases 1 to 1683)  
http://fullileng.cn.invaltogen.com/  
Faraday Avenue  
INVALTGEN CORP. SECTION 200

**AUTHORS** Genoscope.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (20-JUN-2004) Genoscope - Centre National de Séquençage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)  
**COMMENT** - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

FEATURES	Location/Qualifiers
source	1. .1683

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="caxon:9606"
/clone="CS0DM005YB14"
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/plasmid="pCMVSPORT_6"

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ORIGIN

Query Match	Score	DB #	Length
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100.0%	Pred	No	1.2e-82

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1067	100.0%	100.0%	0	0	0	0
1068	100.0%	100.0%	0	0	0	0
1069	100.0%	100.0%	0	0	0	0
1070	100.0%	100.0%	0	0	0	0
1071	100.0%	100.0%	0	0	0	0
1072	100.0%	100.0%	0	0	0	0
1073	100.0%	100.0%	0	0	0	0
1074	100.0%	100.0%	0	0	0	0
1075	100.0%	100.0%	0	0	0	0
1076	100.0%	100.0%	0	0	0	0
1077	100.0%	100.0%	0	0	0	0
1078	100.0%	100.0%	0	0	0	0
1079	100.0%	100.0%	0	0	0	0
1080	100.0%	100.0%	0	0	0	0
1081	100.0%	100.0%	0	0	0	0
1082	100.0%	100.0%	0	0	0	0
1083	100.0%	100.0%	0	0	0	0
1084	100.0%	100.0%	0	0	0	0
1085	100.0%	100.0%	0	0	0	0
1086	100.0%	100.0%	0	0	0	0
1087	100.0%	100.0%	0	0	0	0
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1093	100.0%	100.0%	0	0	0	0
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1098	100.0%	100.0%	0	0	0	0
1099	100.0%	100.0%	0	0	0	0
1100	100.0%	100.0%	0	0	0	0
1101	100.0%	100.0%	0	0	0	0
1102	100.0%	100.0%	0	0	0	0
1103	100.0%	100.0%	0	0	0	0
1104	100.0%	100.0%	0	0	0	0
1105	100.0%	100.0%	0	0	0	0
1106	100.0%	100.0%	0	0	0	0
1107	100.0%	100.0%	0	0	0	0
1108	100.0%	100.0%	0	0	0	0
1109	100.0%	100.0%	0	0	0	0
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1111	100.0%	100.0%	0	0	0	0
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1117	100.0%	100.0%	0	0	0	0
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1119	100.0%	100.0%	0	0	0	0
1120	100.0%	100.0%	0	0	0	0
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1122	100.0%	100.0%	0	0	0	0
1123	100.0%	100.0%	0	0	0	0
1124	100.0%	100.0%	0	0	0	0
1125	100.0%	100.0%	0	0	0	0

[illegible][illegible]

Dd	1202 TATCAGCGGACCTACTGCATTCCAATTCAGAACCCCTGGTAAATCATTTCAATAAATTAATTTTAAAA
Gy	1130 GATGAGATCGAGTACATCTTTCAGGCCATCTGTGTGCCCCCTGAATGGCGATGGCGGGGGCTTG

Db 1262 GATGATCAGTACATCTTCAAGCCATCCTGTGTGCCCTGATGCCATGCGGGGGCTGC 132



GenCore version 5.1.9  
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## OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 23:31:11 ; Search time 2107 Seconds

(without alignments)  
8788.546 Million cell updates/sec

Title: US-10-765-580-11

Perfect score: 1507

Sequence: 1 atgcaccatcatcatcatca.....gtgacaagccagcggtga 1507

Scoring table: IDENTITY NUC

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications NA Main:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1507	100.0	1507	8	US-10-765-580-11
2	881.4	58.5	2073	3	US-09-334-477-46
3	879.4	58.4	2127	3	US-09-334-477-32
4	879	58.3	879	8	US-10-765-580-9
5	878.4	58.3	981	3	US-09-334-477-36
6	877.4	58.2	948	16	US-11-010-795-27
7	877.4	58.2	48908	6	US-10-114-170-137
8	877.2	58.2	1241	3	US-09-334-477-9
9	876.8	58.2	945	3	US-09-334-477-1
10	876.8	58.2	969	3	US-09-334-477-20
11	498.4	33.1	502	9	US-10-425-821-93
12	498	33.0	498	8	US-10-765-580-10
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20	498	33.0	576	8	US-10-384-339C-121	Sequence 121, App
21	498	33.0	576	9	US-10-851-074-2	Sequence 2, Appl1
22	498	33.0	576	9	US-10-714-449-2	Sequence 2, Appl1
23	498	33.0	576	9	US-10-868-577A-6	Sequence 6, Appl1
24	498	33.0	576	15	US-11-116-698-1	Sequence 1, Appl1
25	498	33.0	605	7	US-10-189-360-2	Sequence 2, Appl1
26	498	33.0	649	3	US-09-349-954A-1	Sequence 1, Appl1
27	498	33.0	649	3	US-09-307-007-1	Sequence 1, Appl1
28	498	33.0	649	6	US-10-262-538-19	Sequence 19, Appl1
29	498	33.0	649	7	US-10-170-385-228	Sequence 228, App
30	498	33.0	649	7	US-10-172-118-906	Sequence 906, App
31	498	33.0	649	8	US-10-673-708-1	Sequence 1, Appl1
32	498	33.0	649	8	US-10-342-887-906	Sequence 906, App
33	498	33.0	649	10	US-10-669-176-19	Sequence 19, Appl1
34	498	33.0	649	10	US-10-848-755A-114	Sequence 11, App
35	498	33.0	649	15	US-11-075-400-1	Sequence 1, Appl1
36	498	33.0	658	9	US-10-425-784-1	Sequence 1, Appl1
37	498	33.0	658	9	US-10-848-646-1	Sequence 1, Appl1
38	498	33.0	990	3	US-09-880-107-2336	Sequence 2336, Ap
39	498	33.0	990	3	US-09-795-006A-1	Sequence 1, Appl1
40	498	33.0	990	6	US-10-200-050-1	Sequence 1, Appl1
41	498	33.0	990	6	US-10-155-785-9	Sequence 9, Appl1
42	498	33.0	990	6	US-10-207-655-50	Sequence 50, Appl1
43	498	33.0	990	7	US-10-101-510-53	Sequence 53, Appl1
44	498	33.0	990	7	US-10-131-985-18	Sequence 18, Appl1
45	498	33.0	990	9	US-10-772-927A-11	Sequence 11, Appl1

## ALIGNMENTS

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RESULT 1
US-10-765-580-11
; Sequence 11, Application US/10765580
; Publication No. US20040165565A1
GENERAL INFORMATION:
; APPLICANT: Backer, Joseph M.
; TITLE OF INVENTION: RECOMBINANT PROTEINS CONTAINING
; TITLE OF INVENTION: SHIGA-LIKE TOXIN AND VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 102108-300
; CURRENT APPLICATION NUMBER: US/10/765,580
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/796,861
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/190,973
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ. ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1507
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-765-580-11
Query Match 100.0%; Score 1507; DB 8; Length 1507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 ATGCACCATCATCATCATCTTTCTTGTGCTGCGCCAGCGGTTCTGATGAAGAA 60  
DB 1 ATGCACCATCATCATCATCTTTCTTGTGCTGCGCCAGCGGTTCTGATGAAGAA 60  
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61 ACCGCTGCTGAATTAATTCAGACGACGACATGACAGCCAGATTCGAAAGAAATTAA 120  
DB 61 ACCGCTGCTGAATTAATTCAGACGACGACATGACAGCCAGATTCGAAAGAAATTAA 120  
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D	b	121	TTAGACTTCTGCAGCTGCAGAAACGTAATGTAGATTGCTGAATGTCATTCCGCTCTGCATA	180
O	y	181	GGTACTCCATTACAGACTATTTCATCAGAGGTACGTCCTTACTGATGATTGATAGTGCC	240
D	b	181	GGTACTCCATTACAGACTATTTCATCAGAGGTACGTCCTTACTGATGATTGATAGTGCC	240
O	y	241	ACAGGGGATTAATTTGTTTGAGTGTGAGTGCAGAGGATAGTCCAGAGGAAAGGCGGTT	300
D	b	241	ACAGGGGATTAATTTGTTTGAGTGTGAGTGCAGAGGATAGTCCAGAGGAAAGGCGGTT	300
O	y	301	AATAATCTACGGCTTATTTGTTGAAAGAAATTAATTAATATGTGACAGGATTTGTTAACG	360
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O	y	421	GGCGTTACATTTGCTGTCGTCAGTACGATATACACAGTTACAGCGTGTGTGACGGGATCAGT	480
D	b	421	GGCGTTACATTTGCTGTCGTCAGTACGATATACACAGTTACAGCGTGTGTGACGGGATCAGT	480
O	y	481	CGTACGGGGATGACAGATTAATCCGACTTCGTTGACTACTCTTATCTGATTTAATGTGC	540
D	b	481	CGTACGGGGATGACAGATTAATCCGACTTCGTTGACTACTCTTATCTGATTTAATGTGC	540
O	y	541	CATATGTGAACCTCACTGACGACGTCGTGSCAGAGAGCATGTACCGTATTTGTTACTGTG	600
D	b	541	CATATGTGAACCTCACTGACGACGTCGTGSCAGAGAGCATGTACCGTATTTGTTACTGTG	600
O	y	601	ACAGCTGAAGCTTTACGTTTTCCGCAAAATACAGAGGGGATTTCCGTACAAACCTGATGAT	660
D	b	601	ACAGCTGAAGCTTTACGTTTTCCGCAAAATACAGAGGGGATTTCCGTACAAACCTGATGAT	660
O	y	661	CTCAGTGGGCGCTTCTATGTATATGACGTCGCTGAAGTGTGTACTTACATTTGAATCGGGGA	720
D	b	661	CTCAGTGGGCGCTTCTATGTATATGACGTCGCTGAAGTGTGTACTTACATTTGAATCGGGGA	720
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D	b	721	AGGTTGAGTGAAGCGTCCGCTGACTCATCATGAGACAGACTCTGTTGCTGTAGGAAGAATT	780
O	y	781	TCTTTTGGAAAGCATTAATGCAATTTCTGGAAAGCGTGAATTAAATCTGAATTTGTCATCAT	840
D	b	781	TCTTTTGGAAAGCATTAATGCAATTTCTGGAAAGCGTGAATTAAATCTGAATTTGTCATCAT	840
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D	b	841	CATGCATCGCAGATTGCCAGAAATGSCATCTATGATGTTCCCTTCATGTGTCGCGCAGAT	900
O	y	901	GGAGAAGTCCGTTGGATTACGCACAATAAATATTGTGGATTTCAATCCACTCTGTGGGGCA	960
D	b	901	GGAGAAGTCCGTTGGATTACGCACAATAAATATTGTGGATTTCAATCCACTCTGTGGGGCA	960
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D	b	961	ATTTCGATCGCGAGAACTATTAGCAGTGGGTCCGACGACGACGACGAAGGACCCATGCG	1020
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D	b	1021	AGAAAGAGAGGGCAGAAATCATACGAAAGTGGTGAAGTTCAATGATGTCTATCAGCGCAG	1080
O	y	1081	CTACTGCCATTCGAATGCAAGCCCTGCTGCAACTCTTCCAGAGATACCTGTAGTAGATGCA	1140
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D	b	1201	GGGCTGAGTGTGTGCCCACTGAGAGATTCAAATCACATGCAATTAATCCGATACAA	1266

Db	1201	GGGGCTGGAGATGTGTGCCCACTAGAGGTCMAATCACCATGACGATVTGCGGATCAAA	1260
QY	1261	ACCTTCACCAAGGCCACAGACATAGAGAGATGAGACTTCTCTACAGACAACAAATGTGATG	1320
Db	1261	ACCTTCACCAAGGCCACAGACATAGAGAGATGAGAGCTTCTCTACAGACAACAAATGTGATG	1320
QY	1321	CAGACCCAAAGAAAGATGTAGACCAAGACAAGAAAAATCCCTGTGGGGCTTGTCTCAGAGCCGAG	1380
Db	1321	CAGACCCAAAGAAAGATGTAGACCAAGACAAGAAAAATCCCTGTGGGGCTTGTCTCAGAGCCGAG	1380
QY	1381	AAAGCATTTGTTGTCTACAAGATCCGACGAGGTGTAAATGTTCCTCGCAAAAAACACAGACTC	1440
Db	1381	AAAGCATTTGTTGTCTACAAGATCCGACGAGGTGTAAATGTTCCTCGCAAAAAACACAGACTC	1440
QY	1441	GGCGTTGCAGAGCGAGGACGAGCTTGAGTTAAACGAACGTACTTGCAGATGTGTCAAGACCCGAG	1500
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QY	1501	GGCGGTGA 1507	
Db	1501	GGCGGTGA 1507	

## RESULT 2

US-09-334-477-46  
; Sequence 46, Application US/09334477  
; Patent No. US20020012658A1

GENERAL INFORMATION:

APPLICANT: Williams, James A.

Byrne, Lisa M.  
Byrne, Charles S. G.

pugh, Charles S.C.  
ATTORNEY AT LAW. Preventive

# Verotoxin-Induced Disease

NUMBER OF SEQUENCES: 49

## CORRESPONDENCE ADDRESS:

ADDRESS: Medlen

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California  
COUNTRY: United States of America

COUNTRY: United States of America  
 EID: 04704

ZIP: 94104  
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:  
MEDIUM TYPE: F]only disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

## APPLICATION NUMBER: US/0

FILING DATE: 16-Jun-1999

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;
.CLASSIFICATION: <Unknown>
EDITOR ADDITION DATA:

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PRIOR APPLICATION DATA: 00 0015 0377

APPLICATION NUMBER: 08  
FILING DATE: <Unknown>

FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

NAME: macnigill, nathaniel l.  
REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: OPHD-02450

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-841

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

TYPE: nucleic acid

TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

## DES

FEATURE:

## NAME

LOC .....

SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-09-334-477-46

Query Match	58.5%;	Score 881.4;	DB 3;	Length 2073;
Best Local Similarity	99.3%;	Pred. No. 1.3e-260;		
Matches 885; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

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QY	159	GAATGTCAATTTGCTCTCTGCAATAGTACTCCATTCACAGCTAATTTTCATCAGAGGTACGTC	218
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QY	219	TTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	278
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QY	459	ACAGCGTTTSCAGGGATCACTCGTACGGGAGTCAGATTAATGCGCATTCGTTGACTAC	518
Db	1542	ACAGCGTTTSCAGGGATCACTCGTACGGGAGTCAGATTAATGCGCATTCGTTGACTAC	1601
QY	519	TTCTTATCTGGATTTAATGTCGCATATGGAACCTCACTGACGAGTCTGTCGCAAGGC	578
Db	1602	TTCTTATCTGGATTTAATGTCGCATATGGAACCTCACTGACGAGTCTGTCGCAAGGC	1661
QY	579	GATGTTCAGGTTTGTATCTGTGACACGCTGAAGCTTATTCGCGCAATATACAGAGGG	638
Db	1662	GATGTTCAGGTTTGTATCTGTGACACGCTGAAGCTTATTCGCGCAATATACAGAGGG	1721
QY	639	ATTTCGTATACACACTGAGATGATCTTCAGTGGGCGTTCTATATGTAATGATCTGTCGAAGAT	698
Db	1722	ATTTCGTATACACACTGAGATGATCTTCAGTGGGCGTTCTATATGTAATGATCTGTCGAAGAT	1781
QY	699	TGATCTTTCATATGAACTGGGAGAGGTTGAGTAGCGTCTGCTGACTATACGACACA	758
Db	1782	TGATCTTTCATATGAACTGGGAGAGGTTGAGTAGCGTCTGCTGACTATACGACACA	1841
QY	759	CTCTGTTCTGTAGGAGAAATTTCTTTTGGAACTTAATGCAATTCCTGGGAAGCTGGC	818
Db	1842	CTCTGTTCTGTAGGAGAAATTTCTTTTGGAACTTAATGCAATTCCTGGGAAGCTGGC	1901
QY	819	ATTATATCTGAATGTCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT	878
Db	1902	ATTATATCTGAATGTCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT	1961
QY	879	TCCTTCTATATGTCGCGCAGATGGAAGAGTCGTCGGGATTTACGCAATAAATATTTGTG	938
Db	1962	TCCTTCTATATGTCGCGCAGATGGAAGAGTCGTCGGGATTTACGCAATAAATATTTGTG	2022
QY	939	GGATTTCATCCACTCTGGGGGGAATTCGATGCGGAATCTATACACTG 989	
Db	2022	GGATTTCATCCACTCTGGGGGGAATTCGATGCGGAATCTATACACTG 2072	

RESULT 3  
US-09-334-477-32  
; Sequence 32, Application US/09334477  
; Patent NO. US20020012558A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, James A.  
; Byrne, Lisa M.

[illegible]

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 QY 521 CTTATCTGATTTAATGTCGATAGTGAACCTCACTGACGAGTCTGTGCGAAGCGA 580  
 Db 1658 CTTATCTGATTTAATGTCGATAGTGAACCTCACTGACGAGTCTGTGCGAAGCGA 1717  
 QY 581 TGTTCAGGTTTGTACTGTGACAGCTGAAGCTTTAGCTTTTGGCAATACAGAGGAT 640  
 Db 1718 TGTTCAGGTTTGTACTGTGACAGCTGAAGCTTTAGCTTTTGGCAATACAGAGGAT 1777  
 QY 641 TTGTCACACACGATGATGATCTGAGGCGTTCCTTAATGATGATGATGATGATG 700  
 Db 1778 TTGTCACACACGATGATGATCTGAGGCGTTCCTTAATGATGATGATGATGATG 1837  
 QY 701 ATCTTACATTTGAACTGGGGAAGGTTGAGTACGCTGCTGCTGATCTATCTGACAACT 760  
 Db 1838 ATCTTACATTTGAACTGGGGAAGGTTGAGTACGCTGCTGCTGATCTATCTGACAACT 1897  
 QY 761 CTTGTCGTGAGGAATTTCTTTTGGAACTTAATGCAATTCGCGGGAAGCGTGGCAT 820  
 Db 1898 CTTGTCGTGAGGAATTTCTTTTGGAACTTAATGCAATTCGCGGGAAGCGTGGCAT 1957  
 QY 821 TAATACGATTTGTCATCATCATGATCGGAGTTGCGAATGCGATCTGATGATGTC 880  
 Db 1958 TAATACGATTTGTCATCATCATGATCGGAGTTGCGAATGCGATCTGATGATGTC 2017  
 QY 881 CTTCTATGTCGCGGAGATGGAAGTCCGTGGGATTAAGCAATTAATATTTGTGGG 940  
 Db 2018 CTTCTATGTCGCGGAGATGGAAGTCCGTGGGATTAAGCAATTAATATTTGTGGG 2077  
 QY 941 ATTCATCCACTCTGGGGGCAATCTGATGCGGCAATCTATTAGCACTGG 989  
 Db 2078 ATTCATCCACTCTGGGGGCAATCTGATGCGGCAATCTATTAGCACTGG 2126

## RESULT 4

US-10-765-580-9  
 ; Sequence 9, Application US/10765580  
 ; Publication No. US2004016565A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Backer, Marina V.  
 ; APPLICANT: Backer, Joseph M.  
 ; TITLE OF INVENTION: RECOMBINANT PROTEINS CONTAINING  
 ; TITLE OF INVENTION: SHIGA-LIKE TOXIN AND VASCULAR ENDOTHELIAL GROWTH FACTOR  
 ; TITLE OF INVENTION: FRAGMENTS  
 ; FILE REFERENCE: 102108-300  
 ; CURRENT APPLICATION NUMBER: US/10/765,580  
 ; CURRENT FILING DATE: 2004-01-27  
 ; PRIOR APPLICATION NUMBER: 09/796,861  
 ; PRIOR FILING DATE: 2001-03-01  
 ; PRIOR APPLICATION NUMBER: 60/190,973  
 ; PRIOR FILING DATE: 2000-03-22  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 879  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-765-580-9

Query Match 58.3%; Score 879; DB 8; Length 879;

Best Local Similarity 100.0%; Pred. No. 4,4e-260;

Matches 879; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 AAGGATTTACCTTAGACTTCTGACGCAAGACGATGATGATGATGATGATGATG 60  
 QY 169 CGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 228  
 Db 61 CGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120  
 QY 229 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 288

Db 121 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180  
 QY 289 GAAGGCGGTTTAAATCTACGCTTATGTTTGAAGAAATATTTATATGATGACGGA 348  
 Db 181 GAAGGCGGTTTAAATCTACGCTTATGTTTGAAGAAATATTTATATGATGACGGA 240  
 QY 349 TTTGTTAACGGAATTAATGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTTTAA 408  
 Db 241 TTTGTTAACGGAATTAATGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTTTAA 300  
 QY 409 CCAGTACACACGCGTTTACATTTCTGTCGACAGTACATTAATGATGATGATGATG 468  
 Db 301 CCAGTACACACGCGTTTACATTTCTGTCGACAGTACATTAATGATGATGATGATG 360  
 QY 469 GCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 528  
 Db 361 GCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
 QY 529 GATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 588  
 Db 421 GATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
 QY 589 TTTGTTACTGACAGCTGAAAGCTTTTACGTTTGGGCAATACAGAGGATTTGTCAC 648  
 Db 481 TTTGTTACTGACAGCTGAAAGCTTTTACGTTTGGGCAATACAGAGGATTTGTCAC 540  
 QY 649 ACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 708  
 Db 541 ACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
 QY 709 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 768  
 Db 601 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 QY 769 GTAGGAAGAAATTTCTTTTGAAGCAATTAATGCAATTTCTGGGAAGGCTGCAATTAATG 828  
 Db 661 GTAGGAAGAAATTTCTTTTGAAGCAATTAATGCAATTTCTGGGAAGGCTGCAATTAATG 720  
 QY 829 AATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 888  
 Db 721 AATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 780  
 QY 889 TGTCCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 948  
 Db 781 TGTCCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840  
 QY 949 ACTCTGGGGCAATTTCTGATGCGGCAATTAATGATGATGATGATGATGATG 987  
 Db 841 ACTCTGGGGCAATTTCTGATGCGGCAATTAATGATGATGATGATGATGATG 879

## RESULT 5

US-09-334-477-36

; Sequence 36, Application US/09334477

; Patent No. US20020012658A1

; GENERAL INFORMATION:

; APPLICANT: Williams, James A.

; Pugh, Charles S.G.

; TITLE OF INVENTION: Prevention And Treatment Of

; Verotoxin-Induced Disease

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/334,477  
FILING DATE: 16-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/816,977  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: OPND-02450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 981 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..981  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-334-477-36

Query Match 58.3%; Score 878.4; DB 3; Length 981;  
Best Local Similarity 97.2%; Pred. No. 7,2e-260;  
Matches 894; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

70 GCTAATTCGACGCGCAGACATGACGCCAGATCTGAAGATTACCTTACACTTC 129  
Db 61 GCTGACTCAAGAGGACGATGACAGAGAGCTGTAATTCAGAGATTACCTTACACTTC 120  
Qy 130 TCGACTGCAAGAGCTATGTATGATATCGCTGAATGTCATTCGCTCTGCAATAGTACTCA 189  
Db 121 TCGACTGCAAGAGCTATGTATGATATCGCTGAATGTCATTCGCTCTGCAATAGTACTCA 180  
Qy 190 TTACAGACTATTCATCAGAGAGGATGCTCTTACTGATGATGATGATGACAGAGGAT 249  
Db 181 TTACAGACTATTCATCAGAGAGGATGCTCTTACTGATGATGATGATGACAGAGGAT 240  
Qy 250 AATTTGTTGACGTTGATGTCAGAGGATGATTCAGAGAGAGGCGGTTTAAATATCTA 309  
Db 241 AATTTGTTGACGTTGATGTCAGAGGATGATTCAGAGAGAGGCGGTTTAAATATCTA 300  
Qy 310 CGGCTATTTGTTGAACGAATATTTATATGTCAGAGATTTGTTAAACAGCAAAATAT 369  
Db 301 CGGCTATTTGTTGAACGAATATTTATATGTCAGAGATTTGTTAAACAGCAAAATAT 360  
Qy 370 GTTTTATTCGCTTGTGCTGATTTTTCACATGTTTACCTTCCAGGTACCAAGCGGTTTCA 429  
Db 361 GTTTTATTCGCTTGTGCTGATTTTTCACATGTTTACCTTCCAGGTACCAAGCGGTTTCA 420  
Qy 430 TTGTCGTGACAGTAGCTATACACGTTACAGCGGTTTGACAGGATCAGTGTGACGAGG 489  
Db 421 TTGTCGTGACAGTAGCTATACACGTTACAGCGGTTTGACAGGATCAGTGTGACGAGG 480  
Qy 490 ATGCGATTAATTCGCTATTCGTTGACTATTTCTTATCTGAGATTTAAATGTCGATAGTGA 549  
Db 481 ATGCGATTAATTCGCTATTCGTTGACTATTTCTTATCTGAGATTTAAATGTCGATAGTGA 540  
Qy 550 ACCCTACAGACGCACTCTGTGCAAGAGGATGTTTACGCTTGTGTAAGTGAACAGCTGA 609  
Db 541 ACCCTACAGACGCACTCTGTGCAAGAGGATGTTTACGCTTGTGTAAGTGAACAGCTGA 600  
Qy 610 GCTTACGTTTTCGCAAAATACAGAGGAGATTTTCTTAAACAGCTGATGATCTCAGTGGG 669  
Db 601 GCTTACGTTTTCGCAAAATACAGAGGAGATTTTCTTAAACAGCTGATGATCTCAGTGGG 660

Qy 670 CGTCTATGATTAATGACTGCTGAAGATGTTGATCTTATCAATGAAGTGGGAGGTTGAGT 729  
Db 661 CGTCTATGATTAATGACTGCTGAAGATGTTGATCTTATCAATGAAGTGGGAGGTTGAGT 720  
Qy 730 AGGCTCTGCTGCTGACTATCATGACAGCAAGACTCTGTTGTTGTTAGAGAAATTTCTTTTGA 789  
Db 721 AGGCTCTGCTGCTGACTATCATGACAGCAAGACTCTGTTGTTGTTAGAGAAATTTCTTTTGA 780  
Qy 790 AGCATTAATCAATTTGCGAAGCGTGCGATTAATCACTGAATTTGTCATCATCATCG 849  
Db 781 AGCATTAATCAATTTGCGAAGCGTGCGATTAATCACTGAATTTGTCATCATCATCG 840  
Qy 850 CGAGTTCGCAAGATGCGATGATGATGCTTCTTATGATGTCGCGAGATGGAAGATC 909  
Db 841 CGAGTTCGCAAGATGCGATGATGATGCTTCTTATGATGTCGCGAGATGGAAGATC 900  
Qy 910 CGTGGATTAACGACCAATAAATTTGAGATTCATTCACCTGCGGCGCAATTCGATG 969  
Db 901 CGTGGATTAACGACCAATAAATTTGAGATTCATTCACCTGCGGCGCAATTCGATG 960  
Qy 970 CGCAGAACTATTAGCACTGG 989  
Db 961 CGCAGAACTATTAGCACTGG 980

RESULT 6  
US-11-010-795-27  
Sequence 27, Application US/11010795  
Publication No. US2006005271A1  
GENERAL INFORMATION:  
APPLICANT: TUMER, NILGUN E.  
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE  
FILE REFERENCE: OCIRS 3.0-085  
CURRENT APPLICATION NUMBER: US/11/010,795  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: 60/529,348  
PRIOR FILING DATE: 2003-12-12  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 27  
LENGTH: 948  
TYPE: DNA  
ORGANISM: Bacteriophage SC370  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1) ..(945)  
US-11-010-795-27

Query Match 58.2%; Score 877.4; DB 16; Length 948;  
Best Local Similarity 99.3%; Pred. No. 1.4e-259;  
Matches 881; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 103 GATCGAAGGAATTTACCTTGTGACTCTGCACTGCAAGAGATGATGATTTGCTGAT 162  
Db 61 GTTGGAGGAATTTACCTTGTGACTCTGCACTGCAAGAGATGATGATTTGCTGAT 120  
Qy 163 GTCATTCGCTCTGCAATAGTACTTCATCAGACTAATTTTCATCAGAGGATGCTTTTA 222  
Db 121 GTCATTCGCTCTGCAATAGTACTTCATCAGACTAATTTTCATCAGAGGATGCTTTTA 180  
Qy 223 CTGATGATGATGATGTCAGAGGAGATTAATTTGTTGAGTGTGTCAGAGGAGATGAT 282  
Db 181 CTGATGATGATGATGTCAGAGGAGATTAATTTGTTGAGTGTGTCAGAGGAGATGAT 240  
Qy 283 CCAGAGGAAGGCGGTTTAAATATCTACGCTTATTTGTTGAACAAATTAATTTATG 342  
Db 241 CCAGAGGAAGGCGGTTTAAATATCTACGCTTATTTGTTGAACAAATTAATTTATG 300  
Qy 343 ACAGGATTTGTTAAACAGCAAAATATGTTTTTATGCTTTGCTGATTTTTCACATGTT 402  
Db 301 ACAGGATTTGTTAAACAGCAAAATATGTTTTTATGCTTTGCTGATTTTTCACATGTT 360

403 ACCCTTCCAGTACAAACAGCGGTTACATTTGCTGTGACAGTAGCTATACACGTTACAG 462  
 361 ACCCTTCCAGTACAAACAGCGGTTACATTTGCTGTGACAGTAGCTATACACGTTACAG 420  
 463 CGGTGGAGGAGTACGTGCTACGCGGAGTACAGTAAATCGCATTCGCTGCTACTTCT 522  
 421 CGGTGGAGGAGTACGTGCTACGCGGAGTACAGTAAATCGCATTCGCTGCTACTTCT 480  
 523 TATCTGATTTAATGTCGATAGTGAACCTCACTACGACGAGTCTGTGCAAGACGATG 582  
 481 TATCTGATTTAATGTCGATAGTGAACCTCACTACGACGAGTCTGTGCAAGACGATG 540  
 583 TTAAGGTTTGTATCTGTGACAGCTGAAGCTTTACGTTTTCGCAATAACAGAGGAGATT 642  
 541 TTAAGGTTTGTATCTGTGACAGCTGAAGCTTTACGTTTTCGCAATAACAGAGGAGATT 600  
 643 CGTACAACTGATATCTCACTGAGGCGGCTTCTATGTAATGATGCTGTAAGATGTGAT 702  
 601 CGTACAACTGATATCTCACTGAGGCGGCTTCTATGTAATGATGCTGTAAGATGTGAT 660  
 703 CTACATTTGAACCTGAGGAGGTTGAGTACGCTGCTGCTGATCATGACAGACTCT 762  
 661 CTACATTTGAACCTGAGGAGGTTGAGTACGCTGCTGCTGATCATGACAGACTCT 720  
 763 GTTCGTGTAGAGAAATTTCTTTTGAAGCATTAATGCAATTCGTGGAAGCGTGGCATTA 822  
 721 GTTCGTGTAGAGAAATTTCTTTTGAAGCATTAATGCAATTCGTGGAAGCGTGGCATTA 780  
 823 ATACTGAATTTGATCATCATGATGCGCGAGTTGCGAGAAATGAGCATCTGATGATTTCT 882  
 781 ATACTGAATTTGATCATCATGATGCGCGAGTTGCGAGAAATGAGCATCTGATGATTTCT 840  
 883 TCTATGTCCTGCGACAGATGAGAGATCGTGGGATTAACGCAATTAATTTGGGAT 942  
 841 TCTATGTCCTGCGACAGATGAGAGATCGTGGGATTAACGCAATTAATTTGGGAT 900  
 943 TCATCCACTCTGGGGCAATTCCTGATGCCGACAACTTAATGACAGTTG 989  
 901 TCATCCACTCTGGGGCAATTCCTGATGCCGACAACTTAATGACAGTTG 947

RESULT 7  
 US-10-114-170-137/C  
 ; Sequence 137, Application US/10114170  
 ; Publication No. US2003023075A1  
 GENERAL INFORMATION:  
 APPLICANT: Blatner, Frederick R.  
 Burland, Valerie  
 Perna, Nicole T.  
 Plunkett, Guy  
 Welch, Rod  
 TITLE OF INVENTION: No. US2003023075A1 Sequences of E. coli O157  
 NUMBER OF SEQUENCES: 265  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Charles & Brady  
 STREET: 1 South Pinckney Street  
 CITY: Madison  
 STATE: WI  
 COUNTRY: US  
 ZIP: 53701-2113  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Word Perfect 8.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/114,170  
 FILING DATE: 01-Apr-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/453,702  
 FILING DATE: 03-DEC-1999

APPLICATION NUMBER: 60/110,955  
 FILING DATE: 04-DEC-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seay, Nicholas J.  
 REGISTRATION NUMBER: 27386  
 REFERENCE/DOCKET NUMBER: 960296.95017  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (608) 251-5000  
 TELEFAX: (608) 251-9166  
 INFORMATION FOR SEQ ID NO: 137:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 48908  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Query Match: 58.2% Score 877.4; DB 6; Length 48908;  
 Best Local Similarity 99.3%; Pred. No. 1.5e-258;  
 Matches 881; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

103 GATCTGAAGAAATTACCTTAGACTTTCGACTGCACTGCAAAAGACGTATGATTCGCTGAT 162  
 30777 GTTGGAAAGAAATTACCTTAGACTTTCGACTGCAAAAGACGTATGATTCGCTGAT 30718  
 163 GTCAATTCCTGCTGCAATAGTATCTCCATTAAAGACTATTTGATCAGAGGATACCTTA 222  
 30717 GTCAATTCCTGCTGCAATAGTATCTCCATTAAAGACTATTTGATCAGAGGATACCTTA 30658  
 223 CTGATGATTTGATAGTGGACAGAGGAGTAAATTTGTTTGGATGATGTCAGAGGATAGAT 282  
 30657 CTGATGATTTGATAGTGGACAGAGGAGTAAATTTGTTTGGATGATGTCAGAGGATAGAT 30598  
 283 CCAGAGAAAGGCGGTTTAAATATCTATGATGCTTATTTGTAACGAATTAATTAATGTG 342  
 30597 CCAGAGAAAGGCGGTTTAAATATCTATGATGCTTATTTGTAACGAATTAATTAATGTG 30538  
 343 AAGAGATTTGTTAAACAGACAAATATGTTTTTATCGCTTGTGATTTTACATGTT 402  
 30537 AAGAGATTTGTTAAACAGACAAATATGTTTTTATCGCTTGTGATTTTACATGTT 30478  
 403 ACCCTTCCAGTACAAACAGCGGTTACATTTGCTGTGACAGTAGCTATACACGTTACAG 462  
 30477 ACCCTTCCAGTACAAACAGCGGTTACATTTGCTGTGACAGTAGCTATACACGTTACAG 30418  
 463 CGGTGGAGGAGTACGTGCTACGCGGAGTACAGTAAATCGCATTCGCTGCTACTTCT 522  
 30417 CGGTGGAGGAGTACGTGCTACGCGGAGTACAGTAAATCGCATTCGCTGCTACTTCT 30358  
 523 TATCTGATTTAATGTCGATAGTGAACCTCACTACGACGAGTCTGTGCAAGACGATG 582  
 30357 TATCTGATTTAATGTCGATAGTGAACCTCACTACGACGAGTCTGTGCAAGACGATG 30298  
 583 TTAAGGTTTGTATCTGTGACAGCTGAAGCTTTACGTTTTCGCAATAACAGAGGAGATT 642  
 30297 TTAAGGTTTGTATCTGTGACAGCTGAAGCTTTACGTTTTCGCAATAACAGAGGAGATT 30238  
 643 CGTACAACTGATATCTCACTGAGGCGGCTTCTATGTAATGATGCTGTAAGATGTGAT 702  
 30237 CGTACAACTGATATCTCACTGAGGCGGCTTCTATGTAATGATGCTGTAAGATGTGAT 30178  
 703 CTACATTTGAACCTGAGGAGGTTGAGTACGCTGCTGCTGATCATGACAGACTCT 762  
 30177 CTACATTTGAACCTGAGGAGGTTGAGTACGCTGCTGCTGATCATGACAGACTCT 30118  
 763 GTTCGTGTAGAGAAATTTCTTTTGAAGCATTAATGCAATTCGTGGAAGCGTGGCATTA 822  
 30117 GTTCGTGTAGAGAAATTTCTTTTGAAGCATTAATGCAATTCGTGGAAGCGTGGCATTA 30058  
 823 ATACTGAATTTGATCATCATGATGCGCGAGTTGCGAGAAATGAGCATCTGATGATTTCT 882

Db 30057 ATACTGATTCATCATCATCATCGAGTTGCCAGATGCGATCTTGCT 29998  
Qy 883 TCTATGTGTCGGCAGATGGAAGAGTCCGTGGATTACGCACATTAATTTGGGAT 942  
Db 29997 TCTATGTGTCGGCAGATGGAAGAGTCCGTGGATTACGCACATTAATTTGGGAT 29938  
Qy 943 TCATCAGCTCTGGGGCAATTTGATGCGCAGAACTATTAGAGTGG 989  
Db 29937 TCATCAGCTCTGGGGCAATTTGATGCGCAGAACTATTAGAGTGG 29891

RESULT 8  
US-09-334-477-9  
; Sequence 9, Application US/09334477  
; Patent No. US20020012658A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, James A.  
; Byrne, Lisa M.  
; Pugh, Charles S.G.  
; TITLE OF INVENTION: Prevention And Treatment Of  
; Verotoxin-Induced Disease  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medien & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/334,477  
; FILING DATE: 16-Jun-1999  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/816,977  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Karin T.  
; REGISTRATION NUMBER: 38,230  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1241 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-334-477-9

Query Match 58.2%; Score 877.2; DB 3; Length 1241;  
Best Local Similarity 99.7%; Pred. No. 1.9e-259;  
Matches 879; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 108 GAAGAAATTACTTAGACTTTCGACCTGCAAGAGCTATGTAGATTTCGCTGAATTCAT 167  
Db 66 GAAGAAATTACTTAGACTTTCGACCTGCAAGAGCTATGTAGATTTCGCTGAATTCAT 125  
Qy 168 TCGCTCGCAATAGTACTTCATACAGACTATTTTCATGAGAGTACGCTTTACTGAT 227  
Db 126 TCGCTCGCAATAGTACTTCATACAGACTATTTTCATGAGAGTACGCTTTACTGAT 185  
Qy 228 GATTGATAGTGCACAGAGGGAATATTTGTTGCGAGTTGATGTCAGAGGATAGATCCAGA 287  
Db 186 GATTGATAGTGCACAGAGGGAATATTTGTTGCGAGTTGATGTCAGAGGATAGATCCAGA 245

Qy 288 GGAAGGCGGTTTAATAATCTACGGCTTAATGTTGAAGAAATTAATTATGACAGG 347  
Db 246 GGAAGGCGGTTTAATAATCTACGGCTTAATGTTGAAGAAATTAATTATGACAGG 305  
Qy 348 ATTGTTAACAGAGCAATAATATGTTTATTCGCTTTCGATTTTTCACATGTTACCTT 407  
Db 306 ATTGTTAACAGAGCAATAATATGTTTATTCGCTTTCGATTTTTCACATGTTACCTT 365  
Qy 408 TCCAGGTACAAACAGCGGTTACATTGCTGTGACAGTACTATACAGCTTACAGCGGT 467  
Db 366 TCCAGGTACAAACAGCGGTTACATTGCTGTGACAGTACTATACAGCTTACAGCGGT 425  
Qy 468 TGCAGGATCAGTGTGTCAGGAGTGCAGATTAATGCGATTCGTTACTACTTATCT 527  
Db 426 TGCAGGATCAGTGTGTCAGGAGTGCAGATTAATGCGATTCGTTACTACTTATCT 485  
Qy 528 GGATTTAATGTCGATGATGGAACCTCAGTACCGCAGTCTGTGCAAGAGGATGTTACG 587  
Db 486 GGATTTAATGTCGATGATGGAACCTCAGTACCGCAGTCTGTGCAAGAGGATGTTACG 545  
Qy 588 GTTGTACTGTGACAGCTGAAGCTTTACGTTTTCGCAATACAGAGGGATTTCCATC 647  
Db 546 GTTGTACTGTGACAGCTGAAGCTTTACGTTTTCGCAATACAGAGGGATTTCCATC 605  
Qy 648 AACACTGATGATCTCAGTGGGCGTCTTATGATATGACCTGTAAGATGTTGATCTTAC 707  
Db 606 AACACTGATGATCTCAGTGGGCGTCTTATGATATGACCTGTAAGATGTTGATCTTAC 665  
Qy 708 ATTGAACCTGGAAGGTTGATGATGCTGCTGCTGATCATGATGACAAAGCTGTTCCG 767  
Db 666 ATTGAACCTGGAAGGTTGATGATGCTGCTGCTGATCATGATGACAAAGCTGTTCCG 725  
Qy 768 TGTGGAAGAAATTTCTTTGGAAGCATTAATGCAATTTGCGAAGCGTGGCATTAATCT 827  
Db 726 TGTGGAAGAAATTTCTTTGGAAGCATTAATGCAATTTGCGAAGCGTGGCATTAATCT 785  
Qy 828 GAATTCATCATATCATGATGCGGAGTTCGCAAGATGCGATCTGATGATTTCTTCTAT 887  
Db 786 GAATTCATCATATCATGATGCGGAGTTCGCAAGATGCGATCTGATGATTTCTTCTAT 845  
Qy 888 GTGTCGGCAGATGGAAGAGTCCGTGGATTAACGCAATAAATATTTGGGATTCATC 947  
Db 846 GTGTCGGCAGATGGAAGAGTCCGTGGATTAACGCAATAAATATTTGGGATTCATC 905  
Qy 948 CACTCTGGGGCAATTTCTGATGCGGAGAACTATTAGCAGTGG 989  
Db 906 CACTCTGGGGCAATTTCTGATGCGGAGAACTATTAGCAGTGG 947

RESULT 9  
US-09-334-477-1  
; Sequence 1, Application US/09334477  
; Patent No. US20020012658A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, James A.  
; Byrne, Lisa M.  
; Pugh, Charles S.G.  
; TITLE OF INVENTION: Prevention And Treatment Of  
; Verotoxin-Induced Disease  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medien & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30



CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/334,477  
FILING DATE: 16-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/816,977  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: OPHD-02450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 945 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..945  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-334-477-1

Query Match 58.2%; Score 876.8; DB 3; Length 945;  
Best Local Similarity 99.8%; Pred. No. 2.2e-259;  
Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

108 GAAGAATTACCTTACCTTCTGACGCAAGACGATGTGATTCGCTGATGATCAT 167  
166 GAAGAAATTTACCTTACCTTCTGACGCAAGACGATGTGATTCGCTGATGATCAT 125  
168 TCGCTCGCAATAGTATCTCCATTACAGACTATTTATCAGAGATGATTCATGAT 227  
126 TCGCTCGCAATAGTATCTCCATTACAGACTATTTATCAGAGATGATTCATGAT 185  
228 GATTATAGTGCACAGAGATATTTGTTGAGTGCAGTGCAGAGATGATTCATGAT 287  
186 GATTATAGTGCACAGAGATATTTGTTGAGTGCAGTGCAGAGATGATTCATGAT 245  
288 GGAAGGCGGTTTATATCTACAGGCTTATTTGTTGAGTGCAGTGCAGAGATGAT 347  
246 GGAAGGCGGTTTATATCTACAGGCTTATTTGTTGAGTGCAGTGCAGAGATGAT 305  
348 ATTTGTTACAGACCAATATATGTTTTTATCGCTTGTGATTTTCACTGTTACCTT 407  
306 ATTTGTTACAGACCAATATATGTTTTTATCGCTTGTGATTTTCACTGTTACCTT 365  
408 TCCAGGTACAAACGCGGTTTATGTTGTTGAGTGCAGTGCAGAGATGATTCATGAT 467  
366 TCCAGGTACAAACGCGGTTTATGTTGTTGAGTGCAGTGCAGAGATGATTCATGAT 425  
468 TGCAGGATCATGTCGATGAGGATGAGATTAATCGCATTCGTTGATCTTCTTATCT 527  
426 TGCAGGATCATGTCGATGAGGATGAGATTAATCGCATTCGTTGATCTTCTTATCT 485  
528 GGAATTTATGTCGATGAGGATGAGATTAATCGCATTCGTTGATCTTCTTATCT 587  
486 GGAATTTATGTCGATGAGGATGAGATTAATCGCATTCGTTGATCTTCTTATCT 545  
588 GTTGTACTGTCAGCTGAAAGCTTACGTTTGGCAATATAGAGGGGATTTGTTAC 647  
546 GTTGTACTGTCAGCTGAAAGCTTACGTTTGGCAATATAGAGGGGATTTGTTAC 605  
648 AACACTGATGATCTAGTGGCGTTCTTATGATGATGATGATGATGATGATGATGAT 707  
606 AACACTGATGATCTAGTGGCGTTCTTATGATGATGATGATGATGATGATGATGAT 665  
708 ATTAACTGGGGAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 767

Db 666 ATTGAACGTGGGGAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 725  
Qy 768 TGTAGAAAGATTTCTTTTGAAGCTTATGCAATTTTGGGAAGCGTGGCATTTACT 827  
Db 726 TGTAGAAAGATTTCTTTTGAAGCTTATGCAATTTTGGGAAGCGTGGCATTTACT 785  
Qy 828 GAATGTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 887  
Db 786 GAATGTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 845  
Qy 888 GTGTCCGAGATGAGAGTCTGTTGAGTATGCAATTAATTAATTTGTGGATTCATC 947  
Db 846 GTGTCCGAGATGAGAGTCTGTTGAGTATGCAATTAATTAATTTGTGGATTCATC 905  
Qy 948 CACTGTGGGGAATTCGATGCGGCAATCTTATGACAT 987  
Db 906 CACTGTGGGGAATTCGATGCGGCAATCTTATGACAT 945

## RESULT 10

US-09-334-477-20

Sequence 20, Application US/09334477

Patent No. US20020012658A1

GENERAL INFORMATION:

APPLICANT: Williams, James A.

Byrne, Lisa M.

Pugh, Charles S.G.

TITLE OF INVENTION: Prevention And Treatment Of

Verotoxin-Induced Disease

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSER: Medlen &amp; Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/334,477

FILING DATE: 16-Jun-1999

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/816,977

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: OPHD-02450

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 969 base-pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..969

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-334-477-20

Query Match 58.2%; Score 876.8; DB 3; Length 969;  
Best Local Similarity 99.8%; Pred. No. 2.2e-259;  
Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



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QY 108 GAAGGAATTACTTAGACTTCTGACGTCGAAGAAGCATATGATTTGGCTGATATGTCAT 167
DB 66 GAAGGAATTACTTAGACTTCTGACGTCGAAGAAGCATATGATTTGGCTGATATGTCAT 125
QY 168 TCGCTCTGCAATAGGACTTCATTCACATCTATTCATCAGAGGATAGCTCTTTACTGAT 227
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QY 228 GATTGATATGTCACACAGGAGATTAATTTGTTTGCAGTTGATGTCAGAGGATATGATCCAGA 287
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QY 288 GGAAGGGGGGTTTAATTAATCTACGGCTATTTGTTTGAAGAAATATTTATATATGTCACAGG 347
DB 246 GGAAGGGGGGTTTAATTAATCTACGGCTATTTGTTTGAAGAAATATTTATATATGTCACAGG 305
QY 348 ATTGTTTAAACAGACAAATAATGTTTTTATCGTTTGTGATTTTTCACATGTTACCTT 407
DB 306 ATTGTTTAAACAGACAAATAATGTTTTTATCGTTTGTGATTTTTCACATGTTACCTT 365
QY 408 TCCAGGTACAAACAGCGGTTACATTGTCTGTGACAGTATACCACTTACCTTACTTACT 467
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QY 468 TGCAGGATTCAGTGTAGCGGGATGTCAGATTAATGSCCATTCGTTGACTTACTTACTTACT 527
DB 426 TGCAGGATTCAGTGTAGCGGGATGTCAGATTAATGSCCATTCGTTGACTTACTTACTTACT 485
QY 528 GGATTTAAATGTCGATAGTGAACCTCACTGACGAGTCTGTGACAGAGGATGTTACG 587
DB 486 GGATTTAAATGTCGATAGTGAACCTCACTGACGAGTCTGTGACAGAGGATGTTACG 545
QY 588 GTTGTGTACTGTGACAGCTGAAGCTTTAGCTTTGCGCAATAACAGAGGGGATTTGCTTAC 647
DB 546 GTTGTGTACTGTGACAGCTGAAGCTTTAGCTTTGCGCAATAACAGAGGGGATTTGCTTAC 605
QY 648 AACACTGATGATCTCAGTGGGCGTTCTTATGATATGACTGTCGAAGATGTTGATCTTAC 707
DB 606 AACACTGATGATCTCAGTGGGCGTTCTTATGATATGACTGTCGAAGATGTTGATCTTAC 665
QY 708 ATTGAAGTGGGAGAGTTGAGTAGGCTCTGCTGACTATCATGACAAAGACTCTGTTGCG 767
DB 666 ATTGAAGTGGGAGAGTTGAGTAGGCTCTGCTGACTATCATGACAAAGACTCTGTTGCG 725
QY 768 TGTAGGAAGAAATTTCTTTTGAAGCATTAATGCAATTCGCGAAGCGTGGCATTAATACT 827
DB 726 TGTAGGAAGAAATTTCTTTTGAAGCATTAATGCAATTCGCGAAGCGTGGCATTAATACT 785
QY 828 GAATGTGATCATCATGATCGCGAGTTGCCAGATGTCATCTGATGAGTTTCCCTTAT 887
DB 786 GAATGTGATCATCATGATCGCGAGTTGCCAGATGTCATCTGATGAGTTTCCCTTAT 845
QY 888 GTGTCCGCGACATGAGAGAGTCCGTGGGATTAACGACATTAATAATATGCGGATTCATC 947
DB 846 GTGTCCGCGACATGAGAGAGTCCGTGGGATTAACGACATTAATAATATGCGGATTCATC 905
QY 948 CACTTGTGGGGCAATTTCTGATGCGGACAACTATTAACGCT 987
DB 906 CACTTGTGGGGCAATTTCTGATGCGGACAACTATTAACGCT 945

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RESULT 11
US-10-425-821-93
; Sequence 93, Application US/10425821
; Publication No. US20040219530A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Jos,e
; APPLICANT: BEKAL, Sadjia
; TITLE OF INVENTION: ARRAY AND USERS THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/10/425,821
; CURRENT FILING DATE: 2003-04-30

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; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 93
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-425-821-93

Query Match      33.1%; Score 498.4; DB 9; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.5e-142;
Matches 499; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 108 GAAGGAATTACTTAGACTTCTGACGTCGAAGAAGCATATGATTTGGCTGATATGTCAT 167
DB 3 GAAGGAATTACTTAGACTTCTGACGTCGAAGAAGCATATGATTTGGCTGATATGTCAT 62
QY 168 TCGCTCTGCAATAGGACTTCATTCACATCTATTCATCAGAGGATAGCTCTTTACTGAT 227
DB 63 TCGCTCTGCAATAGGACTTCATTCACATCTATTCATCAGAGGATAGCTCTTTACTGAT 122
QY 228 GATTGATATGTCACACAGGAGATTAATTTGTTTGAAGAAATATTTATATATGTCACAGG 287
DB 123 GATTGATATGTCACACAGGAGATTAATTTGTTTGAAGAAATATTTATATATGTCACAGG 182
QY 288 GGAAGGGGGGTTTAATTAATCTACGGCTATTTGTTTGAAGAAATATTTATATATGTCACAGG 347
DB 183 GGAAGGGGGGTTTAATTAATCTACGGCTATTTGTTTGAAGAAATATTTATATATGTCACAGG 242
QY 348 ATTGTTTAAACAGACAAATAATGTTTTTATCGTTTGTGATTTTTCACATGTTACCTT 407
DB 243 ATTGTTTAAACAGACAAATAATGTTTTTATCGTTTGTGATTTTTCACATGTTACCTT 302
QY 408 TCCAGGTACAAACAGCGGTTACATTGTCTGTGACAGTATACCACTTACCTTACTTACT 467
DB 303 TCCAGGTACAAACAGCGGTTACATTGTCTGTGACAGTATACCACTTACCTTACTTACT 362
QY 468 TGCAGGATTCAGTGTAGCGGGATGTCAGATTAATGSCCATTCGTTGACTTACTTACTTACT 527
DB 363 TGCAGGATTCAGTGTAGCGGGATGTCAGATTAATGSCCATTCGTTGACTTACTTACTTACT 422
QY 528 GGATTTAAATGTCGATAGTGAACCTCACTGACGAGTCTGTGACAGAGGATGTTACG 587
DB 423 GGATTTAAATGTCGATAGTGAACCTCACTGACGAGTCTGTGACAGAGGATGTTACG 482
QY 588 GTTGTGTACTGTGACAGCTG 607
DB 483 GTTGTGTACTGTGACAGCTG 502

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RESULT 12
US-10-765-580-10
; Sequence 10, Application US/10765580
; Publication No. US20040166565A1
; GENERAL INFORMATION:
; APPLICANT: Backer, Marina V.
; APPLICANT: Backer, Joseph M.
; TITLE OF INVENTION: RECOMBINANT PROTEINS CONTAINING
; TITLE OF INVENTION: SHIGA-LIKE TOXIN AND VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 102108-300
; CURRENT APPLICATION NUMBER: US/10/765,580
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/796,861
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/190,973
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Human
US-10-765-580-10

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Query Match 33.0%; Score 498; DB 8; Length 498;  
Best Local Similarity 100.0%; Pred. No. 2e-142;  
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCCATGCGAGAGAGAGAGAGAGAGAGATCATCAGAGTGTGAAGTTCATGATGTG 1069  
DB 1 GCACCCATGCGAGAGAGAGAGAGAGAGATCATCAGAGTGTGAAGTTCATGATGTG 60  
QY 1070 TATCAGCGAGCTACTGCTGCTCAATTCAGAGACCTGTGTGACATCTTCCAGAGTACCTT 1129  
DB 61 TATCAGCGAGCTACTGCTGCTCAATTCAGAGACCTGTGTGACATCTTCCAGAGTACCTT 120  
QY 1130 GATGAGATGAGTACATCTTCAAGCCATCTGTGTGCTGCTGATGAGTGTGAGTGTG 1189  
DB 121 GATGAGATGAGTACATCTTCAAGCCATCTGTGTGCTGCTGATGAGTGTGAGTGTG 180  
QY 1190 TGCATGAT 1249  
DB 181 TGCATGAT 240  
QY 1250 ATGCGGATCAAACTTCACCAAGGCGAGCATATGAGAGATGAGCTTCTTACAGCAAC 1309  
DB 241 ATGCGGATCAAACTTCACCAAGGCGAGCATATGAGAGATGAGCTTCTTACAGCAAC 300  
QY 1310 AAATGTGAATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1369  
DB 301 AAATGTGAATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 360  
QY 1370 TCAGAGCGAT 1429  
DB 361 TCAGAGCGAT 420  
QY 1430 AACACAGACTCGGCTTGCAGAGGCGAGGAGCTTGAAGTAAAGCAAGTACTTGCAGATG 1489  
DB 421 AACACAGACTCGGCTTGCAGAGGCGAGGAGCTTGAAGTAAAGCAAGTACTTGCAGATG 480  
QY 1490 GACACGCCGAGGCGGTGA 1507  
DB 481 GACACGCCGAGGCGGTGA 498

## RESULT 13

US-09-932-451A-1  
; Sequence 1, Application US/09932451A  
; Patent No. US20020111324A1  
; GENERAL INFORMATION:  
; APPLICANT: OZAWA, Keiya  
; APPLICANT: SHIMPO, Masahisa  
; APPLICANT: IKEDA, Yuchi  
; APPLICANT: MAEDA, Yoshikazu  
; APPLICANT: SHIMADA, Kazuyuki  
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-MEDIATED DELIVERY OF ANGIOGENIC  
; FILE REFERENCE: 0800-0026  
; CURRENT APPLICATION NUMBER: US/09/932.451A  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,056  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 576  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-165  
; NAME/KEY: CDS  
; LOCATION: (1)..(576)  
US-09-932-451A-1

Query Match 33.0%; Score 498; DB 3; Length 576;  
Best Local Similarity 100.0%; Pred. No. 2.2e-142;

Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCCATGCGAGAGAGAGAGAGAGAGATCATCAGAGTGTGAAGTTCATGATGTG 1069  
DB 79 GCACCCATGCGAGAGAGAGAGAGAGAGATCATCAGAGTGTGAAGTTCATGATGTG 138  
QY 1070 TATCAGCGAGCTACTGCTGCTCAATTCAGAGACCTGTGTGACATCTTCCAGAGTACCTT 1129  
DB 139 TATCAGCGAGCTACTGCTGCTCAATTCAGAGACCTGTGTGACATCTTCCAGAGTACCTT 198  
QY 1130 GATGAGATGAGTACATCTTCAAGCCATCTGTGTGCTGCTGATGAGTGTGAGTGTG 1189  
DB 199 GATGAGATGAGTACATCTTCAAGCCATCTGTGTGCTGCTGATGAGTGTGAGTGTG 258  
QY 1190 TGCATGAT 1249  
DB 259 TGCATGAT 318  
QY 1250 ATGCGGATCAAACTTCACCAAGGCGAGCATATGAGAGATGAGCTTCTTACAGCAAC 1309  
DB 319 ATGCGGATCAAACTTCACCAAGGCGAGCATATGAGAGATGAGCTTCTTACAGCAAC 378  
QY 1310 AAATGTGAATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1369  
DB 379 AAATGTGAATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 438  
QY 1370 TCAGAGCGAT 1429  
DB 439 TCAGAGCGAT 498  
QY 1430 AACACAGACTCGGCTTGCAGAGGCGAGGAGCTTGAAGTAAAGCAAGTACTTGCAGATG 1489  
DB 499 AACACAGACTCGGCTTGCAGAGGCGAGGAGCTTGAAGTAAAGCAAGTACTTGCAGATG 558  
QY 1490 GACACGCCGAGGCGGTGA 1507  
DB 559 GACACGCCGAGGCGGTGA 576

## RESULT 14

US-10-083-817-8  
; Sequence 8, Application US/10083817  
; Publication No. US20020193288A1  
; GENERAL INFORMATION:  
; APPLICANT: Schreiner, George F.  
; APPLICANT: Johnson, Richard J.  
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
; FILE REFERENCE: SCIOS.002C1  
; CURRENT APPLICATION NUMBER: US/10/083,817  
; CURRENT FILING DATE: 2002-02-26  
; PRIOR APPLICATION NUMBER: 60/099,694  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 09/392,932  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 576  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-083-817-8

Query Match 33.0%; Score 498; DB 6; Length 576;  
Best Local Similarity 100.0%; Pred. No. 2.2e-142;  
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCCATGCGAGAGAGAGAGAGAGATCATCAGAGTGTGAAGTTCATGATGTG 1069  
DB 79 GCACCCATGCGAGAGAGAGAGAGAGATCATCAGAGTGTGAAGTTCATGATGTG 138  
QY 1070 TATCAGCGAGCTACTGCTGCTCAATTCAGAGACCTGTGTGACATCTTCCAGAGTACCTT 1129

Db	139	TATCAGCCAGCTACTGCAATCGAAGACCTGTGTGAACATCTTCAGAGTACCT	198
Qy	1130	GATGAGATCGAGTACTATCTTCAAGCAATCCGTGTGCCCTGATGCGAATGGGGGGCTGC	1189
Db	199	GATGAGATCGAGTACTATCTTCAAGCAATCTGTGTGCCCTGATGCGAATGGGGGGCTGC	258
Qy	1190	TGCAATGACGAGGGGCGTGAAGTGTGTGCCCATGAGAGTCCAAATCAATCAGATG	1249
Db	259	TGCATGACGAGGGGCGTGAAGTGTGTGCCCATGAGAGTCCAAATCAATCAGATG	318
Qy	1250	ATGCGGATCAAACTTCACCAAGGCGAGCATATGAGAGATGAGCTTCCATACAGCAAC	1309
Db	319	ATGCGGATCAAACTTCACCAAGGCGAGCATATGAGAGATGAGCTTCCATACAGCAAC	378
Qy	1310	AAATGTGAATGAGACCAAAAGAAATATGAGGAAGAAAGAAATCCCTGTGGGCGCTTC	1369
Db	379	AAATGTGAATGAGACCAAAAGAAATATGAGGAAGAAAGAAATCCCTGTGGGCGCTTC	438
Qy	1370	TCAGAGCGAGAAACATTTGTGTTGTATACAGATTCGCGAGACGTGTAAATGTTCCTGCAAA	1429
Db	439	TCAGAGCGAGAAACATTTGTGTTGTATACAGATTCGCGAGACGTGTAAATGTTCCTGCAAA	498
Qy	1430	AAACACAGACTCGCGTTGCAAGGCGAGGACGCTTGAGTTAAAGAAAGTATCTTGAGATGT	1489
Db	499	AAACACAGACTCGCGTTGCAAGGCGAGGACGCTTGAGTTAAAGAAAGTATCTTGAGATGT	558
Qy	1490	GACAAAGCGAGGCGGTGA	1507
Db	559	GACAAAGCGAGGCGGTGA	576

	RESULT 15	
US-10-268-447-5		
Sequence 5, Application US/10268447		
Publication No. US2003009675A1		
GENERAL INFORMATION:		
APPLICANT: N. Stephen Pollitt		
APPLICANT: Judith A. Abraham		
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR		
TITLE OF INVENTION: VARIANTS		
FILE REFERENCE: SCIOS 004PVL		
CURRENT APPLICATION NUMBER: US/10/268,447		
CURRENT FILING DATE: 2002-10-10		
PRIOR APPLICATION NUMBER: 60/135,312		
PRIOR FILING DATE: 1999-05-20		
PRIOR APPLICATION NUMBER: 09/574,708		
PRIOR FILING DATE: 2000-05-18		
NUMBER OF SEQ ID NOS: 11		
SOFTWARE: FastSeq for Windows Version 4.0		
SEQ ID NO 5		
LENGTH: 576		
TYPE: DNA		
ORGANISM: Homo sapiens		
FEATURE:		
NAME/KEY: CDS		
LOCATION: (1)...(573)		
US-10-268-447-5		
Query Match	33.0%; Score:498; DB 6; Length 576;	
Best Local Similarity	100.0%; Pred. No. 2.2e-142;	
Matches 498; Conservative	100.0%; Mismatches 0; Indels 0; Gaps 0;	
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DB		
79 GCACCCATGGCAGGAAGGAGGGCGAGATCATCGAAGTGGTGAACTTCATGGATGTC		138
OY		
1070 TATCAGCGCAGCTACTGCCTATCAATCGATGAGACCCTGTGTGACATCTTCAGAGAATACCT		11259
DB		
139 TATCAGCGCAGCTACTGCCTATCAATCGAGACCCTGTGTGACATCTTCAGAGAATACCT		198
OY		
1130 CATGAGATGAGTAATATTCTTGCAAGCAATCTGTGTGCCCTGATGCCATGAGGGGGCTGC		11839
DB		
199 CATGAGATGAGTAATATTCTTGCAAGCAATCTGTGTGCCCTGATGCCATGAGGGGGCTGC		258

OY	1190	TGCAATACGAGGGCCGTGGAGTGTGTCCCATGAGAGTCCAACTATCACCATGCAATT	1249
Db	259	TGCAATACGAGGGCCGTGGAGTGTGTCCCATGAGAGTCCAACTATCACCATGCAATT	318
OY	1250	ATGGCGATTCAAACTCTACCAAGGCCACACACTAGAGAGATGAGCTTCTTACAGCACAC	1309
Db	319	ATGGCGATTCAAACTCTACCAAGGCCACACACTAGAGAGATGAGCTTCTTACAGCACAC	378
OY	1310	AAATGTGATTCAGACCCAAAGAAAGATAGACCAAGACAGAAATTCCTGTGGGCTTGC	1365
Db	379	AAATGTGATTCAGACCCAAAGAAAGATAGACCAAGACAAATTCCTGTGGGCTTGC	438
OY	1370	TCAGAGCGAGAAAGCATTTGTTGTATCAAAATCCGAGACGTATAATGTTCCGTGAAA	1422
Db	439	TCAGAGCGAGAAAGCATTTGTTGTATCAAAATCCGAGAGCTATAATGTTCCGTGAAA	498
OY	1430	AAACACAGCTGCGCTGTGCAGGCGAGAGCTTGATTTAAACGAACTACTTGCAGATGT	1488
Db	499	AAACACAGCTGCGCTGTGCAGGCGAGAGCTTGATTTAAACGAACTACTTGCAGATGT	558
OY	1490	GACAAGCCGAGCGCGTGA 1507	
Db	559	GACAAGCCGAGCGCGTGA 576	

Search completed: January 23, 2007, 04:36:37  
Job time : 2111 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

## OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 23:26:15 ; Search time 313 Seconds  
(without alignments)  
9008.821 Million cell updates/sec

Title: US-10-765-580-11

Perfect score: 1507  
Sequence: 1 atgacacatcatcatcatca.....gtgacaaagcgagcggtga 1507

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93555401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents NA: \*  
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3: /EMC\_Celerra\_SIDS3/prodata/2/ina/68 COMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	881.4	58.5	2073	US-08-816-977-46	Sequence 46, Appl
2	881.4	58.5	2073	US-09-334-477-46	Sequence 46, Appl
3	879.4	58.4	2127	US-08-816-977-32	Sequence 32, Appl
4	879.4	58.4	2127	US-09-334-477-32	Sequence 32, Appl
5	878.4	58.3	981	US-08-816-977-36	Sequence 36, Appl
6	878.4	58.3	981	US-09-334-477-36	Sequence 36, Appl
7	877.4	58.2	48908	US-09-453-7028-137	Sequence 137, App
8	877.4	58.2	48908	US-10-114-170-137	Sequence 137, App
9	877.2	58.2	1241	US-08-816-977-9	Sequence 9, Appl
10	877.2	58.2	1241	US-09-334-477-9	Sequence 9, Appl
11	876.8	58.2	945	US-08-816-977-1	Sequence 1, Appl
12	876.8	58.2	945	US-09-334-477-1	Sequence 1, Appl
13	876.8	58.2	969	US-08-816-977-20	Sequence 20, Appl
14	876.8	58.2	969	US-09-334-477-20	Sequence 20, Appl
15	505.8	33.6	1299	PCT-US95-10973A-58	Sequence 58, Appl
16	502.4	33.3	1809	PCT-US95-10973A-79	Sequence 79, Appl
17	498	33.0	576	US-09-392-932-8	Sequence 8, Appl
18	498	33.0	576	US-09-574-708A-5	Sequence 5, Appl
19	498	33.0	576	US-09-392-931-5	Sequence 5, Appl
20	498	33.0	576	US-10-268-447-5	Sequence 5, Appl
21	498	33.0	576	US-10-418-529-5	Sequence 5, Appl
22	498	33.0	605	US-08-718-904-2	Sequence 2, Appl
23	498	33.0	605	US-09-449-249-2	Sequence 2, Appl

24	498	33.0	605	7	PCT-US95-10973A-26	Sequence 26, Appl
25	498	33.0	649	3	US-09-949-016-1168	Sequence 1168, Ap
26	498	33.0	989	10	5332671-11	Patent No. 5332671
27	498	33.0	990	3	US-08-567-200A-1	Sequence 1, Appl
28	498	33.0	990	3	US-08-591-794-1	Sequence 1, Appl
29	498	33.0	990	3	US-08-882-816-1	Sequence 1, Appl
30	498	33.0	990	3	US-08-802-052B-1	Sequence 1, Appl
31	498	33.0	990	4	US-09-795-006A-1	Sequence 1, Appl
32	498	33.0	990	4	US-09-880-107-2336	Sequence 2336, Ap
33	498	33.0	990	5	US-09-346-069-1	Sequence 1, Appl
34	498	33.0	2136	3	US-09-587-184-1	Sequence 1, Appl
35	498	33.0	3583	3	US-09-976-594-921	Sequence 921, App
36	498	33.0	5163	3	US-09-919-039-166	Sequence 166, App
37	498	33.0	5610	3	US-09-655-493B-2	Sequence 2, Appl
38	496.4	32.9	498	10	5194586-20	Patent No. 5194586
39	496.4	32.9	498	10	5219739-21	Patent No. 5219739
40	496.4	32.9	990	3	US-08-734-443-13	Sequence 13, Appl
41	495.2	32.9	1269	7	PCT-US95-10973A-32	Sequence 32, Appl
42	495	32.8	599	7	PCT-US95-10973A-89	Sequence 89, Appl
43	493.4	32.7	1369	7	PCT-US95-10973A-33	Sequence 33, Appl
44	489	32.4	599	7	PCT-US95-10973A-87	Sequence 87, Appl
45	447.6	29.7	961	10	5219739-16	Patent No. 5219739

## ALIGNMENTS

RESULT 1  
US-08-816-977-46  
Sequence 46, Application US/08816977  
Patent No. 6080400  
GENERAL INFORMATION:  
APPLICANT: Williams, James A.  
APPLICANT: Byrne, Lisa M.  
TITLE OF INVENTION: Prevention And Treatment Of  
TITLE OF INVENTION: Verotoxin-Induced Disease  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,977  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2073 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2070  
US-08-816-977-46

Query Match 58.5%; Score 881.4; DB 3; Length 2073;  
 Best Local Similarity 99.3%; Pred. No. 3.7e-273;  
 Matches 885; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 99 CCCAGATCGAAGGATTTTACCTTAGACTTCCTCGCACTGCAAGAGCTATGTAGATTGCT 158
DB 1182 CCCGGAATTCAGAGAAATTTACCTTAGACTTCCTCGCAAGAGCTATGTAGATTGCT 1241
QY 159 GAATGTCATTCGCTCGCAATAGTATCTCCATTAAGACTATTTTCATCAGAGAGTACGTC 218
DB 1242 GAATGTCATTCGCTCGCAATAGTATCTCCATTAAGACTATTTTCATCAGAGAGTACGTC 1301
QY 219 TTTTACTGATGATTGATGAGCAAGAGGATTAATTTGTTGAGATTGATGTCAGAGGAT 278
DB 1302 TTTTACTGATGATTGATGAGCAAGAGGATTAATTTGTTGAGATTGATGTCAGAGGAT 1361
QY 279 AGATCCAGAGGAAGGGCGGTTTAATTAATCTACGGCTTAATGTTGAACGAATTAATTA 338
DB 1362 AGATCCAGAGGAAGGGCGGTTTAATTAATCTACGGCTTAATGTTGAACGAATTAATTA 1421
QY 339 TGTGACAGGATTTGTTAAGAGCAAAATTAATGTTTATCGCTTTCGATTTCACA 398
DB 1422 TGTGACAGGATTTGTTAAGAGCAAAATTAATGTTTATCGCTTTCGATTTCACA 1481
QY 399 TGTTACCTTTCCAGGTACAAACAGCGGTTTCAATTGCTGTGAGCACTAGCTATACAGCTT 458
DB 1482 TGTTACCTTTCCAGGTACAAACAGCGGTTTCAATTGCTGTGAGCACTAGCTATACAGCTT 1541
QY 459 ACAGCGTGTTCAGAGGATCAATGCTGACGGGATGACAGATTAATCCCATTCCTTACTAC 518
DB 1542 ACAGCGTGTTCAGAGGATCAATGCTGACGGGATGACAGATTAATCCCATTCCTTACTAC 1601
QY 519 TTTCTATCTGATTTTAATGTGCAATAGTGAACCTTCACTGACGACAGTCTGTGCAAGAC 578
DB 1602 TTTCTATCTGATTTTAATGTGCAATAGTGAACCTTCACTGACGACAGTCTGTGCAAGAC 1661
QY 579 GATGTTACGGTGTGTTTACCTGACAGCTTAACCTTTTCCGCAAAATTAACAGAGGG 638
DB 1662 GATGTTACGGTGTGTTTACCTGACAGCTTAACCTTTTCCGCAAAATTAACAGAGGG 1721
QY 639 ATTTGCTAGAACACTGAGATGATCTCAGTGGGCGTCTTATGTAATGACTGCTGAAGATGT 698
DB 1722 ATTTGCTAGAACACTGAGATGATCTCAGTGGGCGTCTTATGTAATGACTGCTGAAGATGT 1781
QY 699 TGATCTTACATTAACCTGAGGAAAGTTGAGTAGGCTTCTGCTGACTATCATGAGACAA 758
DB 1782 TGATCTTACATTAACCTGAGGAAAGTTGAGTAGGCTTCTGCTGACTATCATGAGACAA 1841
QY 759 CTCTGTTGCTGTAGGAAGATTTCTTTTGGAGCATTAATGCAATTCGAGGAAGCGTGGC 818
DB 1842 CTCTGTTGCTGTAGGAAGATTTCTTTTGGAGCATTAATGCAATTCGAGGAAGCGTGGC 1901
QY 819 ATTAATAGTGAATTTGATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 878
DB 1902 ATTAATAGTGAATTTGATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1961
QY 879 TCTTTCTATGTTGTCGAGCAGATGGAAGATTCCTGGGATTAAGCAAAATTAATATTGTC 938
DB 1962 TCTTTCTATGTTGTCGAGCAGATGGAAGATTCCTGGGATTAAGCAAAATTAATATTGTC 2021
QY 939 GGATTCATCAGCTCTGGGGGCAATTCGATGCGCAGAACTATTAGCAGTGG 989
DB 2022 GGATTCATCAGCTCTGGGGGCAATTCGATGCGCAGAACTATTAGCAGTGG 2072
  
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RESULT 2  
 US-09-334-477-46  
 ; Sequence 46, Application US/09334477  
 ; Patent No. 6652857  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Williams, James A.  
 ; Byrnie, Lisa M.

Pugh, Charles S.G.

TITLE OF INVENTION: Prevention And Treatment Of  
 Verotoxin-Induced Disease

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medline & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/334,477

FILING DATE: 16-Jun-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/816,977

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: OPD-02450

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 2073 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

MOLECULE TYPE: other nucleic acid

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2070

SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-09-334-477-46

Query Match 58.5%; Score 881.4; DB 3; Length 2073;

Best Local Similarity 99.3%; Pred. No. 3.7e-273;

Matches 885; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

QY 99 CCCAGATCGAAGGATTTTACCTTAGACTTCCTCGCACTGCAAGAGCTATGTAGATTGCT 158
DB 1182 CCCGGAATTCAGAGAAATTTACCTTAGACTTCCTCGCACTGCAAGAGCTATGTAGATTGCT 1241
QY 159 GAATGTCATTCGCTTCGCAATAGTATCTCCATTAAGACTATTTTCATCAGAGAGTACGTC 218
DB 1242 GAATGTCATTCGCTTCGCAATAGTATCTCCATTAAGACTATTTTCATCAGAGAGTACGTC 1301
QY 219 TTTTACTGATGATTGATGAGCAAGAGGATTAATTTGTTGAGATTGATGTCAGAGGAT 278
DB 1302 TTTTACTGATGATTGATGAGCAAGAGGATTAATTTGTTGAGATTGATGTCAGAGGAT 1361
QY 279 AGATCCAGAGGAAGGGCGGTTTAATTAATCTACGGCTTAATGTTGAACGAATTAATTA 338
DB 1362 AGATCCAGAGGAAGGGCGGTTTAATTAATCTACGGCTTAATGTTGAACGAATTAATTA 1421
QY 339 TGTGACAGGATTTGTTAAGAGCAAAATTAATGTTTATCGCTTTCGATTTCACA 398
DB 1422 TGTGACAGGATTTGTTAAGAGCAAAATTAATGTTTATCGCTTTCGATTTCACA 1481
QY 399 TGTTACCTTTCCAGGTACAAACAGCGGTTTCAATTGCTGTGAGCACTAGCTATACAGCTT 458
DB 1482 TGTTACCTTTCCAGGTACAAACAGCGGTTTCAATTGCTGTGAGCACTAGCTATACAGCTT 1541
QY 459 ACAGCGTGTTCAGAGGATCAATGCTGACGGGATGACAGATTAATCCCATTCCTTACTAC 518
  
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Db      1542 ACAGCGTGTGACGGAGTCAGTCGTAACGGGAGTGCAGTAATATGCCATTGCTGACCTAC 1601
Oy      519  TTCTTATCTGCATTTAATGTCCGATAGTGGAACTCTCACTGACGAGTCTGTGGCAAGGC 578
Db      1602 TTCTTATCTGCGATTTTAAATGTCCCAATAGTGGAACTCTCACTGACGCGTCTGTGGCAAGGC 1661
Oy      579  GATGTACGGGTTTGGTAACTGTGACAGCTGAAGCTTTAGGTTTGGGCAAAATACAGAGGG 638
Db      1662 GATGTACGGGTTTGGTAACTGTGACAGCTGAAGCTTTAGGTTTGGGCAAAATACAGAGGG 1721
Oy      639  ATTTCGTAACAACATCGATGATCTCAGTGGCGTTCTTATGTAATGACTGCTGAAGATGT 698
Db      1722 ATTTGTAACAACATCGATGATCTCAGTGGCGTTCTTATGTAATGACTGCTGAAGATGT 1781
Oy      699  TGATCTTACATTTGAATCTGCGGGAAGGTGAGTACGAGTCCGCTGCTGCTATCATGACGA 758
Db      1782 TGATCTTACATTTGAATCTGCGGGAAGGTGAGTACGAGTCCGCTGCTGCTATCATGACGA 1841
Oy      759  CTCTGTCGTGTAGGAGCAATTTCTTTTGGAAAGCAATTAATGCAATCTGGAAGCGTGGC 818
Db      1842 CTCTGTCGTGTAGGAGCAATTTCTTTTGGAAAGCAATTAATGCAATCTGGAAGCGTGGC 1901
Oy      819  ATTAATACGTAATTTGTCATCATCATGATCGGAGTGGCTCCAGATGCGATCTGATGATT 878
Db      1902 ATTAATACGTAATTTGTCATCATCATGATCGGAGTGGCTCCAGATGCGATCTGATGATT 1961
Oy      879  TCCTCTCATGATGTCCGGGAGATGGAAGAGTCCGTGGGATTAAGCAATTAATAATTGTG 938
Db      1962 TCCTCTCATGATGTCCGGGAGATGGAAGAGTCCGTGGGATTAAGCAATTAATAATTGTG 2021
Oy      939  GGATTCATCCACTCTGGGGGCAATTTCTGATGGCGAGAACTAATTACAGACTG 989
Db      2022 GGATTCATCCACTCTGGGGGCAATTTCTGATGGCGAGAACTAATTACAGACTG 2072

RESULT 3
US-08-816-977-32
; Sequence 32, Application US/08816977
; Patent No. 6080400
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Byrne, Lisa M.
; TITLE OF INVENTION: Prevention And Treatment Of
; TITLE OF INVENTION: VeroToxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,977
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Karlin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2127 base pairs

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[illegible]





REFERENCE/DOCKET NUMBER: OPND-02450  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 705-8410  
 TELEFAX: (415) 397-8338  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 981 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..981  
 US-08-816-977-36

Query Match 58.3%; Score 878.4; DB 3; Length 981;  
 Best Local Similarity 97.2%; Pred. No. 2.1e-272;  
 Matches 894; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

70 GCTAAATTCGACCGCAGACATGACAGCCAGATCGAAGAAATTAACCTTAGACTTC 129  
 61 GCTGACTCAAGAGAGACGATGACAGAGCTTGAAATTCAGAAATTAACCTTAGACTTC 120  
 130 TCGACTGCAAGAGACGATGATGATGCTGGAATGCTTCGCTGCAATAGTACTCA 189  
 121 TCGACTGCAAGAGACGATGATGATGCTGGAATGCTTCGCTGCAATAGTACTCA 180  
 190 TTACAGACTATTTCATCAGAGAGTACGCTTTACTGATGATGATGATGAGGAGAT 249  
 181 TTACAGACTATTTCATCAGAGAGTACGCTTTACTGATGATGATGATGAGGAGAT 240  
 250 AATTGTTGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 309  
 241 AATTGTTGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 310 CGGCTTATGTTGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 369  
 301 CGGCTTATGTTGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
 370 GTTATTTATCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 429  
 361 GTTATTTATCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
 430 TTGCTGATGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 489  
 421 TTGCTGATGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 490 ATGAGATTAATCGCATTCGTTGATGATGATGATGATGATGATGATGATGATGATGAT 549  
 481 ATGAGATTAATCGCATTCGTTGATGATGATGATGATGATGATGATGATGATGATGAT 540  
 550 ACCCTACTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 609  
 541 ACCCTACTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 610 GCTTACGTTTCCGCAATACAGAGGGGATTTCTTACAACTGAGATGATGATGATGAT 669  
 601 GCTTACGTTTCCGCAATACAGAGGGGATTTCTTACAACTGAGATGATGATGATGAT 660  
 670 GCTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729  
 661 GCTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
 730 AGCGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 789  
 721 AGCGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 790 AGCATTAATGCAATCTGAGAGCGTGGCAATTAATGATGATGATGATGATGATGATGAT 849  
 781 AGCATTAATGCAATCTGAGAGCGTGGCAATTAATGATGATGATGATGATGATGATGAT 840  
 850 CGAGTTGCGAGAGTGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 909

841 CGAGTTGCGAGAGTGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 910 CGTGGATTAACGCAATTAATTTGTGGATTAATCACTCTGGGGGCAATTCATG 969  
 901 CGTGGATTAACGCAATTAATTTGTGGATTAATCACTCTGGGGGCAATTCATG 960  
 970 CGCAGAACTATTACAGTGG 989  
 961 CGCAGAACTATTACAGTGG 980

RESULT 6  
 US-09-334-477-36  
 Sequence 36.6652857  
 Patent No. 6652857  
 GENERAL INFORMATION:  
 APPLICANT: Williams, James A.  
 Byrnes, Lisa M.  
 Pugh, Charles S.G.  
 TITLE OF INVENTION: Prevention and Treatment Of  
 Verotoxin-Induced Disease  
 NUMBER OF SEQUENCES: 49  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Medlen & Carroll, LLP  
 STREET: 220 Montgomery Street, Suite 2200  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States of America  
 ZIP: 94104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/334,477  
 FILING DATE: 16-Jun-1999  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/816,977  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MacKnight, Kamrin T.  
 REGISTRATION NUMBER: 38,230  
 REFERENCE/DOCKET NUMBER: OPND-02450  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 397-8338  
 TELEFAX: (415) 705-8410  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 981 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..981  
 SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
 US-09-334-477-36

Query Match 58.3%; Score 878.4; DB 3; Length 981;  
 Best Local Similarity 97.2%; Pred. No. 2.1e-272;  
 Matches 894; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

70 GCTAAATTCGACCGCAGACATGACAGCCAGATCGAAGAAATTAACCTTAGACTTC 129  
 61 GCTGACTCAAGAGAGACGATGACAGAGCTTGAAATTCAGAAATTAACCTTAGACTTC 120  
 130 TCGACTGCAAGAGACGATGATGATGCTGGAATGCTTCGCTGCAATAGTACTCA 189  
 121 TCGACTGCAAGAGACGATGATGATGCTGGAATGCTTCGCTGCAATAGTACTCA 180

190 TTACAGACTATTTTCATCAGAGAGTACGCTTTACTGATGATGATGAGGAGAT 249  
181 TTACAGACTATTTTCATCAGAGAGTACGCTTTACTGATGATGATGAGGAGAT 240  
250 AATTTGTTGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 309  
241 AATTTGTTGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
310 CGGCTTATTTGTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 369  
301 CGGCTTATTTGTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 360  
370 GTTTTATTTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 429  
361 GTTTTATTTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 420  
430 TTGCTGTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 489  
421 TTGCTGTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 480  
490 ATGACATTAATTCGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 549  
481 ATGACATTAATTCGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 540  
550 ACCCTGCTGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 609  
541 ACCCTGCTGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
610 GCTTTTATTTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 669  
601 GCTTTTATTTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 660  
670 CGTTTCTTATTTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 729  
661 CGTTTCTTATTTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 720  
730 AGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789  
721 AGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
790 AGCATTAATTCGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 849  
781 AGCATTAATTCGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 840  
850 CGGCTTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 909  
841 CGGCTTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 900  
910 CGTGGGATTTACGCAATAAATTTGTTGATTTCACTCTGCGGAGGCAATTTGATG 969  
901 CGTGGGATTTACGCAATAAATTTGTTGATTTCACTCTGCGGAGGCAATTTGATG 960  
970 CGCAGAACTTATAGCAGTGG 989  
961 CGCAGAACTTATAGCAGTGG 980

RESULT 7  
US-09-453-702B-137/c  
Sequence 137, Application US/09453702B  
Patent No. 6365723  
GENERAL INFORMATION:  
APPLICANT: Blactner, Frederick R.  
Burland, Nicole T.  
Perna, Nicole T.  
Plunkett, Guy  
Welch, Rod  
TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street

CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 8.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,702B  
FILING DATE: 03-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/110,955  
FILING DATE: 04-Dec-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 960296.95017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 251-5000  
TELEFAX: (608) 251-9166  
INFORMATION FOR SEQ ID NO: 137:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48908  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 137:  
US-09-453-702B-137  
Query Match 58.2%; Score 877.4; DB 3; Length 48908;  
Best Local Similarity 99.3%; Pred. No. 5.5e-271;  
Matches 881; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
103 GATCTGAAGAAATTTTACCTTAGACTTCTGACTGCAAGAGATGATGATTCGCGAT 162  
30777 GTTGGGAAGAAATTTTACCTTAGACTTCTGACTGCAAGAGATGATGATTCGCGAT 30718  
163 GTTATTCGCTGCAATAGTACTCTCATTAGAGACTATTTCATCAGAGATGATGATTC 222  
30717 GTTATTCGCTGCAATAGTACTCTCATTAGAGACTATTTCATCAGAGATGATGATTC 30658  
223 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 282  
30657 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 30598  
283 CCAGAGAAAGGCGGTTTAAATCTTACGCGCTTATTTGTTGAAGAAATTAATTTATG 342  
30597 CCAGAGAAAGGCGGTTTAAATCTTACGCGCTTATTTGTTGAAGAAATTAATTTATG 30538  
343 ACAGATTTGTTAACAAGCAAAATATGTTTTTATCGCTTCTGATTTTTCACATGTT 402  
30537 ACAGATTTGTTAACAAGCAAAATATGTTTTTATCGCTTCTGATTTTTCACATGTT 30478  
403 ACCTTCCAGTACAACAGCGGTTTACATTTGCTGATGATGATGATGATGATGATGAT 462  
30477 ACCTTCCAGTACAACAGCGGTTTACATTTGCTGATGATGATGATGATGATGATGAT 30418  
463 CGTGTTCAGAGGATCAGTGTGATGAGGAGTGCATTAATTCGCTTCTGATTTTCT 522  
30417 CGTGTTCAGAGGATCAGTGTGATGAGGAGTGCATTAATTCGCTTCTGATTTTCT 30358  
523 TATCTGATTTAATGTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 582  
30357 TATCTGATTTAATGTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 30298  
583 TTACGCTTTGTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 642  
30297 TTACGCTTTGTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 30238

QY 643 CGTACAACTGATGATCTGAGTGGGCTTCTATGATGATGATGATGATGAT 702  
DB 30237 CGTACAACTGATGATCTGAGTGGGCTTCTATGATGATGATGATGATGAT 30178  
QY 703 CTTACATGAACTGAGGAGGTTGAGTGGGCTTCTGATGATGATGATGATGATGAT 762  
DB 30177 CTTACATGAACTGAGGAGGTTGAGTGGGCTTCTGATGATGATGATGATGATGAT 30118  
QY 763 GTTGTGTAGGAGAAATTTCTTTTGAAGCAATTAATGCAATTTGGAAGGCTGATTA 822  
DB 30117 GTTGTGTAGGAGAAATTTCTTTTGAAGCAATTAATGCAATTTGGAAGGCTGATTA 30058  
QY 823 ATACGAATTTGATCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 882  
DB 30057 ATACGAATTTGATCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 29998  
QY 883 TCTATGTCTCCGCGAGATGAGAGAGTCCGTGGGATTAAGCAATTAATTAATTTGAGAT 942  
DB 29997 TCTATGTCTCCGCGAGATGAGAGAGTCCGTGGGATTAAGCAATTAATTAATTTGAGAT 29938  
QY 943 TCATCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTTG 989  
DB 29937 TCATCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTTG 29891

RESULT 8  
US-10-114-170-137/c  
Sequence 137, Application US/10114170  
Patent No. 6855814

## GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.

Burland, Valerie

Perna, Nicole T.

Melch, Rod

TITLE OF INVENTION: No. 6855814el Sequences of E. coli O157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSER: Charles &amp; Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM: Medium type: Diskette, 3.50 inch, 1.44mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,170

FILING DATE: 01-Apr-2002

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/453,702

FILING DATE: 03-DEC-1999

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296, 95017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-5000

TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 137:

SEQUENCE CHARACTERISTICS:

LENGTH: 48908

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 137:

US-10-114-170-137

Query Match 58.2%; Score 877.4; DB 3; Length 48908;

Best Local Similarity 99.3%; Pred. No. 5.5e-271;

Matches 881; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 103 GATCTGAGGAATTTACCTTAGACTTCTGACATGCAAGAGATGATGATGATGAT 162  
DB 30777 GTTGTGTAGGAGAAATTTCTTTTGAAGCAATTAATGCAATTTGGAAGGCTGATTA 30718  
QY 163 GTATTCGCTCTGCAATAGGATCTCATTAAGCAATTAATTTGATGAGGATGATTA 222  
DB 30717 GTATTCGCTCTGCAATAGGATCTCATTAAGCAATTAATTTGATGAGGATGATTA 30658  
QY 223 CTGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 282  
DB 30657 CTGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 30598  
QY 283 CCAGAGAGAGGCGGTTTAATTAATCTACGCTTAATGTTGACAGAAATTAATTAATG 342  
DB 30597 CCAGAGAGAGGCGGTTTAATTAATCTACGCTTAATGTTGACAGAAATTAATTAATG 30538  
QY 343 ACAGAGATTTGTAACAGACAAATTAATGTTTATGCTTGTGATTTTTCATGTT 402  
DB 30537 ACAGAGATTTGTAACAGACAAATTAATGTTTATGCTTGTGATTTTTCATGTT 30478  
QY 403 ACCTTTCCAGGTACAAACAGCGGTTACATTTGCTGCTGACAGTACTTACACGTTACAG 462  
DB 30477 ACCTTTCCAGGTACAAACAGCGGTTACATTTGCTGCTGACAGTACTTACACGTTACAG 30418  
QY 463 CGTGTTCAGGGATCAGTCTGACGCGGATGAGATTAATGCGCATTTGCTGATCTTCT 522  
DB 30417 CGTGTTCAGGGATCAGTCTGACGCGGATGAGATTAATGCGCATTTGCTGATCTTCT 30358  
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DB 30297 TTAAGCTTTGTTACTGACAGCTGAGGCTTTAGGTTTGGCAATTCAGAGGGGATTT 30238  
QY 643 CGTACAACTGATGATCTGAGTGGGCTTCTATGATGATGATGATGATGATGAT 702  
DB 30237 CGTACAACTGATGATCTGAGTGGGCTTCTATGATGATGATGATGATGATGAT 30178  
QY 703 CTTACATGAACTGAGGAGGTTGAGTGGGCTTCTGATGATGATGATGATGATGAT 762  
DB 30177 CTTACATGAACTGAGGAGGTTGAGTGGGCTTCTGATGATGATGATGATGATGAT 30118  
QY 763 GTTGTGTAGGAGAAATTTCTTTTGAAGCAATTAATGCAATTTGGAAGGCTGATTA 822  
DB 30117 GTTGTGTAGGAGAAATTTCTTTTGAAGCAATTAATGCAATTTGGAAGGCTGATTA 30058  
QY 823 ATACGAATTTGATCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 882  
DB 30057 ATACGAATTTGATCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 29998  
QY 883 TCTATGTCTCCGCGAGATGAGAGAGTCCGTGGGATTAAGCAATTAATTAATTTGAGAT 942  
DB 29997 TCTATGTCTCCGCGAGATGAGAGAGTCCGTGGGATTAAGCAATTAATTAATTTGAGAT 29938  
QY 943 TCATCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTTG 989  
DB 29937 TCATCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTTG 29891

RESULT 9

US-08-816-977-9

Sequence 9, Application US/08816977

Patent No. 6080400

GENERAL INFORMATION:

APPLICANT: Williams, James A.

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APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSER: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1241 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-816-977-9

Query Match      58.2%; Score 877.2; DB 3; Length 1241;
Best Local Similarity 99.7%; Pred. No. 6,1e-272;
Matches 879; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 108 GAAGGAATTTACCTTACCTTCTGACTGCAAGAGCGTATGATGCTGCTGATGCTAT 167
DB 66 GAAGGAATTTACCTTACCTTCTGACTGCAAGAGCGTATGATGCTGCTGATGCTAT 125
QY 168 TCCGCTGCAATGATGCTCTCCATTACGACTATTTTCATCAGAGGATCGCTTACTGAT 227
DB 126 TCCGCTGCAATGATGCTCTCCATTACGACTATTTTCATCAGAGGATCGCTTACTGAT 185
QY 228 GATTGATAGTGCACAGAGGATATTTGTTGAGTTGATGTCAGAGGATAGATCCAGA 287
DB 186 GATTGATAGTGCACAGAGGATATTTGTTGAGTTGATGTCAGAGGATAGATGAGA 245
QY 288 GGAAGCGCGGTTATATATCTAGCGCTTATTTGAAAGAAATATATATATATGACAGG 347
DB 246 GGAAGCGCGGTTATATATCTAGCGCTTATTTGAAAGAAATATATATATATGACAGG 305
QY 348 ATTGTTACAGAGCAATATATGTTTTTATCGCTTGCATTTTTCACATGTTACTCT 407
DB 306 ATTGTTACAGAGCAATATATGTTTTTATCGCTTGCATTTTTCACATGTTACTCT 365
QY 408 TCCAGTACAAACAGCGGTTACATTTGCTGTGTCAGATAGCTATATACCAAGTACAGCGTGT 467
DB 366 TCCAGTACAAACAGCGGTTACATTTGCTGTGTCAGATAGCTATATACCAAGTACAGCGTGT 425
QY 468 TGCAGGATCAGTGTACGCGGATGCGATATATCCGCATTTGTTGACTACTTCTTATCT 527
DB 426 TGCAGGATCAGTGTACGCGGATGCGATATATCCGCATTTGTTGACTACTTCTTATCT 485
QY 528 GGATTTATATGTCGATATGTCGATCCTCAGTACGACGCTGTGTGCAAGAGCGATGTTACG 587
DB 486 GGATTTATATGTCGATATGTCGATCCTCAGTACGACGCTGTGTGCAAGAGCGATGTTACG 545

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QY 588 GTTGTCTACTGTCAGCTGAGAGCTTTACGTTTTCGCGCAAAATACAGAGGAGTTTCGTAC 647
DB 546 GTTGTCTACTGTCAGCTGAGAGCTTTACGTTTTCGCGCAAAATACAGAGGAGTTTCGTAC 605
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QY 708 ATGTAACGAGGAGGTTGAGAGGCTGTCCTGCTGACTATCATGGAACAAGACTGTTCTG 767
DB 666 ATGTAACGAGGAGGTTGAGAGGCTGTCCTGCTGACTATCATGGAACAAGACTGTTCTG 725
QY 768 TGTAGAGAAATTTCTTTTGGAGAGCATTAATGCAATTTGCGAAGCGTGGCATTAATCT 827
DB 726 TGTAGAGAAATTTCTTTTGGAGAGCATTAATGCAATTTGCGAAGCGTGGCATTAATCT 785
QY 828 GAATGTGATCATCATGTCATGCGGAGTGGCCGAGATGGCAATGGCATCTGATGATTTCTTCAT 887
DB 786 GAATGTGATCATCATGTCATGCGGAGTGGCCGAGATGGCAATGGCATCTGATGATTTCTTCAT 845
QY 888 GTGTCCGCGAGATGAGAGGTCCTGCGGATTTACGCAATATAATTTGTGGATTTCAATC 947
DB 846 GTGTCCGCGAGATGAGAGGTCCTGCGGATTTACGCAATATAATTTGTGGATTTCAATC 905
QY 948 CACTCTGGGGCAATTTCTGATGCGGAGAACTATTAGCAATGG 989
DB 906 CACTCTGGGGCAATTTCTGATGCGGAGAACTATTAGCAATGG 947

RESULT 10
US-09-334-477-9
Sequence 9, Application US/09334477
Patent No. 6652857
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSER: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1241 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

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SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-334-477-9

Query Match 58.2%; Score 877.2; DB 3; Length 1241;  
Best Local Similarity 99.7%; Pred. No. 6,1e-272;  
Matches 879; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 108 GAAGGAATTTACCTTACCTTCTGACGCGAAGACGATGATTCGGATGATCAT 167
Db 66 GAAGGAATTTACCTTACCTTCTGACGCGAAGACGATGATTCGGATGATCAT 125
Qy 168 TCGCTTCGCAATAGTACTCCATTTACAGACTATTTCAATCAGAGTACGCTTTACTGAT 227
Db 126 TCGCTTCGCAATAGTACTCCATTTACAGACTATTTCAATCAGAGTACGCTTTACTGAT 185
Qy 228 GATTGATAGTGGCAGAGGGATATTTGTTTGCAGTTGATGTCAGAGGATGATCCAGA 287
Db 186 GATTGATAGTGGCAGAGGGATATTTGTTTGCAGTTGATGTCAGAGGATGATCCAGA 245
Qy 288 GGAAGGGCGGTTTAAATATCTAAGGCTTATGTTGAAGCAATTAATTAATGAGACAG 347
Db 246 GGAAGGGCGGTTTAAATATCTAAGGCTTATGTTGAAGCAATTAATTAATGAGACAG 305
Qy 348 ATTGTTAAACAGACAAATATATGTTTTTATCGCTTGTGATTTTCAATGTTACTCT 407
Db 306 ATTGTTAAACAGACAAATATATGTTTTTATCGCTTGTGATTTTCAATGTTACTCT 365
Qy 408 TCCAGGTACAAACAGCGGTTTACATTTGCTGGTGAAGTACTATACACGCTTGT 467
Db 366 TCCAGGTACAAACAGCGGTTTACATTTGCTGGTGAAGTACTATACACGCTTGT 425
Qy 468 TGCAGGGATCAGTGTGACGGGGATGACATTAATCGCATTCGTTGACTACTTCTTACT 527
Db 426 TGCAGGGATCAGTGTGACGGGGATGACATTAATCGCATTCGTTGACTACTTCTTACT 485
Qy 528 GGATTTAATGTGCAATAGTGAACCTCACTGACGAGCTGTGTGCAAGAGCGATGTTACG 587
Db 486 GGATTTAATGTGCAATAGTGAACCTCACTGACGAGCTGTGTGCAAGAGCGATGTTACG 545
Qy 588 GTTGTGTTACTGTGACAGTGAAGCTTTTACGTTTTCGCAATACAGAGGGATTTCTGAC 647
Db 546 GTTGTGTTACTGTGACAGTGAAGCTTTTACGTTTTCGCAATACAGAGGGATTTCTGAC 605
Qy 648 AACACTGATGATCTCAGTGGGCGTTCTTATGTAATGACCTGCAAGATGTTGATCTTAC 707
Db 606 AACACTGATGATCTCAGTGGGCGTTCTTATGTAATGACCTGCAAGATGTTGATCTTAC 665
Qy 708 ATTGAACCTGGGAAAGTTGAGTACGCTTCCTGACTATCATGACACAGACCTGCTTGC 767
Db 666 ATTGAACCTGGGAAAGTTGAGTACGCTTCCTGACTATCATGACACAGACCTGCTTGC 725
Qy 768 TGTGAGGAAGATTTCTTTGAGACATTAATGCAATTCGTGGAAGCGTGGATTAATACT 827
Db 726 TGTGAGGAAGATTTCTTTGAGACATTAATGCAATTCGTGGAAGCGTGGATTAATACT 785
Qy 828 GAATTCATCATCATGATGATGCGAGTTCAGAGATGATGATGATGATGATGATGAT 887
Db 786 GAATTCATCATCATGATGATGCGAGTTCAGAGATGATGATGATGATGATGATGAT 845
Qy 888 GTGTCCGCGACAGTGAAGAGTCCGTGGGATTTACGCAATTAATTAATGTTGGATGATC 947
Db 846 GTGTCCGCGACAGTGAAGAGTCCGTGGGATTTACGCAATTAATTAATGTTGGATGATC 905
Qy 948 CACTCTGGGGGCAATTCGATGCGCAAGACATTAATGACGCTGG 989
Db 906 CACTCTGGGGGCAATTCGATGCGCAAGACATTAATGACGCTGG 947

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RESULT 11  
US-08-816-977-1  
; Sequence 1, Application US/08816977  
; Patent No. 6080400  
; GENERAL INFORMATION:

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: APPLICANT: Williams, James A.
: APPLICANT: Byrne, Lisa M.
: APPLICANT: Pugh, Charles S.G.
: TITLE OF INVENTION: Prevention And Treatment Of
: TITLE OF INVENTION: Verotoxin-Induced Disease
: NUMBER OF SEQUENCES: 49
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Medlen & Carroll, LLP
: STREET: 220 Montgomery Street, Suite 2200
: CITY: San Francisco
: STATE: California
: COUNTRY: United States of America
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/816,977
: FILING DATE: 13-MAR-1997
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: MacKnight, Kamrin T.
: REGISTRATION NUMBER: 38,230
: REFERENCE/DOCKET NUMBER: OPD-02450
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 705-8410
: TELEFAX: (415) 397-8338
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 945 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..945

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US-08-816-977-1  
Query Match 58.2%; Score 876.8; DB 3; Length 945;  
Best Local Similarity 99.8%; Pred. No. 6,8e-272;  
Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 108 GAAGGAATTTACCTTACCTTCTGACGCGAAGACGATGATTCGGATGATCAT 167
Db 66 GAAGGAATTTACCTTACCTTCTGACGCGAAGACGATGATTCGGATGATCAT 125
Qy 168 TCGCTTCGCAATAGTACTCCATTTACAGACTATTTCAATCAGAGTACGCTTTACTGAT 227
Db 126 TCGCTTCGCAATAGTACTCCATTTACAGACTATTTCAATCAGAGTACGCTTTACTGAT 185
Qy 228 GATTGATAGTGGCAGAGGGATATTTGTTTGCAGTTGATGTCAGAGGATGATCCAGA 287
Db 186 GATTGATAGTGGCAGAGGGATATTTGTTTGCAGTTGATGTCAGAGGATGATCCAGA 245
Qy 288 GGAAGGGCGGTTTAAATATCTAAGGCTTATGTTGAAGCAATTAATTAATGAGACAG 347
Db 246 GGAAGGGCGGTTTAAATATCTAAGGCTTATGTTGAAGCAATTAATTAATGAGACAG 305
Qy 348 ATTGTTAAACAGACAAATATATGTTTTTATCGCTTGTGATTTTCAATGTTACTCT 407
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Qy 408 TCCAGGTACAAACAGCGGTTTACATTTGCTGGTGAAGTACTATACACGCTTGT 467
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RESULT 13  
US-08-816-977-20  
Sequence 20, Application US/08816977  
Patent No. 6080400  
GENERAL INFORMATION:  
APPLICANT: Williams, James A.  
APPLICANT: Byrne, Lisa M.  
APPLICANT: Pugh, Charles S.G.  
TITLE OF INVENTION: Prevention And Treatment Of  
TITLE OF INVENTION: Verotoxin-Induced Disease  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,977  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: OPND-02450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 969 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..969  
US-08-816-977-20  
Query Match 58.2%; Score 876.8; DB 3; Length 969;  
Best Local Similarity 99.8%; Pred. No. 6.9e-272;  
Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 108 GAAGAAATTTACCTTAGACTTCTCGACGCAAGACGATGATGCTGCTGAATGTCAT 167  
DB 66 GAAGAAATTTACCTTAGACTTCTCGACGCAAGACGATGATGCTGCTGAATGTCAT 125  
QY 168 TCGCTCTGCATAGTACTTCCATTACACACTATTTTCATCAGAGAGTACTTCTTACTAT 227  
DB 126 TCGCTCTGCATAGTACTTCCATTACACACTATTTTCATCAGAGAGTACTTCTTACTAT 185  
QY 228 GATTGATAGTGGACAGGAGATTAATTTGTTGACAGTATGTCAGAGGATAGATCCAGA 287  
DB 186 GATTGATAGTGGCTCAGGAGATTAATTTGTTGACAGTATGTCAGAGGATAGATCCAGA 245  
QY 288 GGAAGGGCGGTTTAATTAATCTACGCTTAATGTTGAACGAATAATTAATATGTCACAG 347  
DB 246 GGAAGGGCGGTTTAATTAATCTACGCTTAATGTTGAACGAATAATTAATATGTCACAG 305  
QY 348 ATTTGTTAAACGAGCAAAATTAATGTTTTTATCGCTTGTGATTTTTTACATGTTACCTT 407  
DB 306 ATTTGTTAAACGAGCAAAATTAATGTTTTTATCGCTTGTGATTTTTTACATGTTACCTT 365  
QY 408 TCCAGGTACAAACGCGTTACATGTCGTGTGACAGTAGTACGATTAACAGCTTACAGCTGT 467

DB 366 TCCAGGTACAAACGCGTTACATGTCGTGTGACAGTAGTACGATTAACAGCTTACAGCTGT 425  
QY 468 TCCAGGATCATGTCGATCGGGGATGCAATTAATTCGCATTCCTTACTATCT 527  
DB 426 TCCAGGATCATGTCGATCGGGGATGCAATTAATTCGCATTCCTTACTATCT 485  
QY 528 GGAATTAATGTCGATAGTGAACCTCACTGACGAGCTGTGTGCAAGAGCATGTTACG 587  
DB 486 GGAATTAATGTCGATAGTGAACCTCACTGACGAGCTGTGTGCAAGAGCATGTTACG 545  
QY 588 GTTTGTTACTGTGACAGCTGAACCTTACCTTTTGGCAATAACAGAGGATTTGCTAC 647  
DB 546 GTTTGTTACTGTGACAGCTGAACCTTACCTTTTGGCAATAACAGAGGATTTGCTAC 605  
QY 648 AACACTGATGATCTCAGTGGGCGTTCTTATGTAATGATCGTGGAAATGTCATCTAC 707  
DB 606 AACACTGATGATCTCAGTGGGCGTTCTTATGTAATGATCGTGGAAATGTCATCTAC 665  
QY 708 ATTGAACCTGGGGAAGGTTGATGAGCGCTGCTGCTGATCATGACCAAGACTCTGTTG 767  
DB 666 ATTGAACCTGGGGAAGGTTGATGAGCGCTGCTGCTGATCATGACCAAGACTCTGTTG 725  
QY 768 TGTAGAAAGAAATTTCTTTTGAAGCAATTAATGCAATTTGGGAAAGCGTGCATTAATCT 827  
DB 726 TGTAGAAAGAAATTTCTTTTGAAGCAATTAATGCAATTTGGGAAAGCGTGCATTAATCT 785  
QY 828 GAATTCATCATCATGATCGGAGCTGGGCAAGATGGCATCTGATGAGTTCTCTTAT 887  
DB 786 GAATTCATCATCATGATCGGAGCTGGGCAAGATGGCATCTGATGAGTTCTCTTAT 845  
QY 888 GTGTCGGGCGAGATGGAAGAGTCGCTGGGATTAACGCAATTAATATTTGGGATTCATC 947  
DB 846 GTGTCGGGCGAGATGGAAGAGTCGCTGGGATTAACGCAATTAATATTTGGGATTCATC 905  
QY 948 CACTCTGGGGCAATTTCTGATGCGCAGCACTATTAGCAGT 987  
DB 906 CACTCTGGGGCAATTTCTGATGCGCAGCACTATTAGCAGT 945

RESULT 14  
US-09-334-477-20  
Sequence 20, Application US/09334477  
Patent No. 6652857  
GENERAL INFORMATION:  
APPLICANT: Williams, James A.  
APPLICANT: Byrne, Lisa M.  
APPLICANT: Pugh, Charles S.G.  
TITLE OF INVENTION: Prevention And Treatment Of  
TITLE OF INVENTION: Verotoxin-Induced Disease  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/334,477  
FILING DATE: 16-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/816,977  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230





Search completed: January 23, 2007, 00:58:32  
Job time : 314 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 23:20:43 ; Search time 8793 Seconds  
(without alignments)  
10959.714 Million cell updates/sec

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Gap 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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2: gb\_pat: \*  
3: gb\_ph: \*  
4: gb\_pl: \*  
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7: gb\_sts: \*  
8: gb\_sy: \*  
9: gb\_un: \*  
10: gb\_vl: \*  
11: gb\_ov: \*  
12: gb\_hgt: \*  
13: gb\_in: \*  
14: gb\_om: \*  
15: gb\_ba: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	881.4	58.5	2073	AR431428	AR431428 Sequence
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4	880.4	58.4	1369	E27911	E27911 Method for
5	880.4	58.4	1601	AF461168	AF461168 Escherich
6	880.4	58.4	6921	EC0413275	AJ413275 Bacterioph
7	880.4	58.4	7333	AY638795	AY638795 Stx1-con
8	880.4	58.4	57930	LPH556162	AJ556162 Phase BP-
9	879.6	58.4	6014	SDY271153	AJ271153 Shigella
10	879.4	58.4	2127	AR099884	AR099884 Sequence
11	879.4	58.4	2127	AR431418	AR431418 Sequence
12	879	58.3	1238	AB030485	AB030485 Escherich
13	879	58.3	1362	SS0132761	AJ132761 Shigella
14	879	58.3	1500	SHFSMT	M19437 S. dysenter
15	879	58.3	1956	AF461172	AJ461172 Escherich
16	879	58.3	8053	SS0279086	AJ279086 Shigella
17	879	58.3	32094	AF15317	AF15317 Shigella
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23	878.8	58.3	1905	3	H30SLT	M23980 Bacterioph
24	878.8	58.3	18362	3	AF034975	AF034975 Bacterioph
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#### ALIGNMENTS

RESULT 1  
AR099894  
LOCUS AR099894  
DEFINITION Sequence 46 from patent US 6080400.  
ACCESSION AR099894  
VERSION AR099894.1 GI:12810342  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2073)  
AUTHORS Williams,J.A. and Byrne,L.Marie.  
TITLE Compositions for the prevention and treatment of verotoxin-induced disease  
JOURNAL Patent: US 6080400-A 46 27-JUN-2000;  
FEATURES  
source  
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DB	1242	GAATGTCATTCGCTTCGCAATAGTACTTCATTCAGACTATTCATCAGAGTACGTC	1301		
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QY	279	AGATTCAGAGGAGGCGGTTAATATATATATATATATATATATATATATATATAT	338		
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 LOCUS Sequence 46 from patent US 6652857.  
 DEFINITION AR431428  
 ACCESSION AR431428  
 VERSION AR431428.1 GI:40193464  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 2073)  
 AUTHORS Williams J.A., Byrne L.M. and Pugh C.S.G.  
 TITLE Methods for producing avian verotoxin antitoxin  
 JOURNAL Patent: US 6652857-A 46 25-NOV-2003;  
 Promega Corporation; Madison, WI  
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 DEFINITION toxin 1 B-subunit, complete cds.  
 ACCESSION AB015056  
 VERSION AB015056.1 GI:6527100  
 KEYWORDS shiga-like toxin 1 B-subunit; stx1 B-subunit; shiga-like toxin 1  
 A-subunit; stx1 A-subunit.  
 SOURCE Escherichia coli  
 ORGANISM Escherichia coli  
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 Enterobacteriaceae; Escherichia.  
 REFERENCE 1 (sites)  
 AUTHORS Iwasa M., Makino S., Asakura H., Kobori H. and Morimoto Y.





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Oy	648	AACACTGGATGATCTCAGTGGGCGCTTATATGTAATGATCTGTAAGATGTTGATCTTAC	707
Db	898	AACACTGGATGATCTCAGTGGGCGCTTATATGTAATGATCTGTAAGATGTTGATCTTAC	957
Oy	708	ATTGAACGTGGGAAAGTTGAGTGAAGCGTCTGCTGATCTATCATGAGACAAAGCTCTGTTGG	767
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DEFINITION	Bacteriophage Lahn1 proviral nina gene (partial), ORF92, ORF71, ORF78, ninf gene, ORF175, ninf gene, ORF13, ORF350, ORF51, roi gene, ninf gene, ninf gene, q gene, stx1a gene and stx1b gene (partial).		
ACCESSION	AJ413275.1 GI:23343476		
VERSION	AJ413275.1		
KEYWORDS	late anti-terminator; nina gene; ninf gene; ninf gene; ninf gene; ninf gene; ORF13; ORF350; ORF51; ORF71; ORF78; q gene; recombination endonuclease; roi gene; Roi protein; shiga toxin 1, subunit A; shiga toxin 1, subunit B; stx1a gene; stx1b gene.		
SOURCE	Bacteriophage Lahn1		
ORGANISM	Bacteriophage Lahn1		
REFERENCE	1		
AUTHORS	El-Sayed, A.A.A.		
TITLE	Molecular characterisation of two shiga toxin encoding bacteriophages from enterohaemorrhagic <i>Escherichia coli</i> Thesis (2000) Department of Veterinary Medicine,		
JOURNAL	Justus-Liebig-University, D-35392 Giessen, Germany		
REFERENCE	2		
AUTHORS	El-Sayed, A.A.A., Wietler, L.H., Baljer, G., Stamm, I. and Kroeger, M.		
TITLE	Identification of Shiga toxin producing prophages in <i>E. coli</i> from bovine reveal new insights into toxic phage evolution		
JOURNAL	Unpublished		

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REFERENCE      3 (bases 1 to 6921)
AUTHORS       Kroeger M.
TITLE         Direct Submission
JOURNAL       Submitted (24-SEP-2001) Kroeger M., Inst. f. Mikrobiology and
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              D-35392 Giessen, GERMANY
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VERSION  
KEYWORDS

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Phage BP-4795 complete genome.  
AJ556162 AJ487680  
AJ556162.1 GI:49523585

antigenic protein N; antiterminal protein O; avirulence protein; bet gene; Bet protein; ci gene; cii gene; ciii gene; complete genome; cro gene; dam gene; damage-inducible protein DinI; din gene; DNA; N-6-adenine-methyltransferase Dam; DNA-binding protein Roi; endopeptidase Rz; excisionase; exo gene; exonuclease; gam gene; head-tail adaptor; host-nuclease inhibitor protein Gam; hypothetical protein; hypothetical protein Yhs; int gene; integrase; kil gene; Kil protein; large subunit terminase; low gene; major head protein/prohead protease; major tail subunit; minor tail protein; N gene; nih gene; Nihb protein; nung gene; Ning protein; nih gene; Nihd protein; O gene; outer membrane protein Lm precursor; P gene; pep3 gene; portal protein; O gene; R gene; R protein; regulatory protein CII; regulatory protein CIII; regulatory protein Cro; ren gene; Ren protein; replication protein O; replication protein P; repressor protein Ci; roi gene; Rz gene; S gene; S protein; Shiga toxin 1 subunit A; Shiga toxin 1 subunit B; single-stranded DNA binding component; stxal gene; stxal gene; tail assembly chaperone; tail component; tail fiber component; tail fiber protein; transposase OrfA protein of 15629; transposase OrfB protein of 15629; type III secretion system effector; xis gene; Yhs gene.

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ORGANISM  
REFERENCE  
AUTHORS

Phage BP-4795  
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae; Lambda-like viruses; unclassified Lambda-like viruses.  
Creutzburg, K., Recktenwald, J., Kuhle, V., Herold, S., Hensel, M. and

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TITLE      Schmidt, H.
JOURNAL    The Shiga Toxin 1-Converting Bacteriophage BP-4795 Encodes an
PUBMED     N1a-like Type III Effector Protein
REFERENCE  J. Bacteriol. 187 (24), 8494-8498 (2005)
AUTHORS    16321954
TITLE      2 (bases 1 to 57930)
JOURNAL    Schmidt, H.
            Direct Submission
            Submitted (12-APR-2003) Schmidt H., Institute of Medical
            Microbiology and Hy, Technical University of Dresden,
            Fetscherstrasse 74, D-01307 Dresden, GERMANY
            revised by [3]
            3 (bases 1 to 57930)
REMARK      Direct Submission
AUTHORS     Submitted (06-JUL-2005) Schmidt H., Department of Food
JOURNAL     Microbiology, Institute of Food Technology, University of
            Hohenheim, Garbensenstrasse 28, D-70599 Stuttgart, GERMANY
            On Aug 3, 2005 this sequence version replaced gi:30910914.
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Best Local Similarity 99.7%; Pred. No. 6.7e-252;  
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OY 168 TCGCTTCGCAATAGTACTCTCATTTACAGACTATTTTCATCAGAGGTAGCTTTTACTGAT 227  
DB 1592 TCGCTTCGCAATAGTACTCTCATTTACAGACTATTTTCATCAGAGGTAGCTTTTACTGAT 1651  
OY 228 GATTGATAGTGCACAGGGGATAAATTTGTTGACGTTGATGTCAGAGGATAGATCCAGA 287  
DB 1652 GATTGATAGTGCACAGGGGATAAATTTGTTGACGTTGATGTCAGAGGATAGATCCAGA 1711  
OY 288 GGAAGGCGGCTTAAATCTACCGGCTTATGTTGAAAGAAATATTTATATGACACAG 347  
DB 1712 GGAAGGCGGCTTAAATCTACCGGCTTATGTTGAAAGAAATATTTATATGACACAG 1771  
OY 348 ATTGTTACAGACAAATATATGTTTATCGCTTGCTGATTTTTCACATGTACCTT 407  
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DB 1992 TGCAGGATACAGTGTACCGGGGATGACAGTAAATCGGCATTCGTTACTTCTTACT 1951  
OY 528 GGATTTATATGTCGATAGTGAACCTCAGTCGACGAGCTGTGCAAGAGGATGTTACG 587  
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LOCUS AR099884  
DEFINITION Sequence 32 from patent US 6080400.  
ACCESSION AR099884

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VERSION      AR099884.1  GI:12810332
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 2127)
AUTHORS      Williams, J.A. and Byrne, L.M.
TITLE        Compositions for the prevention and treatment of verotoxin-induced
              disease
JOURNAL      Patent: US 6080400-A 32 27-JUN-2000;
FEATURES     Location/Qualifiers
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              /organism="unknown"
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Best Local Similarity 99.3%; Pred. No. 8.5e-252;
Matches 883; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 101 CAGATCTGAAGAAATTTACTTGAATCTTCTGCACTGCAAGACGATGATGATTCGCTGA 160
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DB 1238 CAGAAATTCAGGAATTTACTTGAATCTTCTGCACTGCAAGACGATGATGATTCGCTGA 1297

QY 161 ATGTCATTCGCTCTGCAATAGTACTCATTACAGACTATTTGATCAGAGGATGCTT 220
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DB 1538 TTACCTTTCCAGGTACAAACGCGTTTACATTTCTGCTGACAGTACTATACACGTTAC 1597

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DB 1598 AGCGTGTGAGGATGATGCTGACAGGGGATGAGATTAATTCGATTCGTTGACTACT 1657

QY 521 CTATCTGATTTAATGTCATAGTGAACCTTCACTGACGACGAGTCTGTGGCAAGCGA 580
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DEFINITION Sequence 32 from patent US 6652857.
ACCESSION AR431418
VERSION    AR431418.1  GI:40193454
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 2127)
AUTHORS    Williams, J.A., Byrne, L.M. and Pugh, C.S.G.
TITLE      Methods for producing avian verotoxin antitoxin
JOURNAL    Patent: US 6652857-A 32 25-NOV-2003;
            Promega Corporation; Madison, WI

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Query Match      58.4%; Score 879.4; DB 2; Length 2127;
Best Local Similarity 99.3%; Pred. No. 8.5e-252;
Matches 883; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 101 CAGATCTGAAGAAATTTACTTGAATCTTCTGCACTGCAAGACGATGATGATTCGCTGA 160
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QY 941 ATTCATCCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTGG 989  
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RESULT 12  
LOCUS AB030485 1238 bp DNA linear BCT 06-JAN-2001  
DEFINITION Escherichia coli stx1 genes for Shiga-like toxin 1 A-subunit, Shiga-like toxin 1 B-subunit, complete cds.  
ACCESSION AB030485.1 GI:12249025  
VERSION AB030485.1  
KEYWORDS Shiga-like toxin 1 B-subunit; Shiga-like toxin 1 A-subunit.  
SOURCE Escherichia coli  
ORGANISM Escherichia coli  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.  
REFERENCE 1 (bases 1 to 1238)  
AUTHORS Sou-ichi, M.  
TITLE Detection of Shiga-like Toxin Producing Escherichia coli from Seagull  
JOURNAL Published Only in Database (2001)  
REFERENCE 2 (bases 1 to 1238)  
AUTHORS Sou-ichi, M.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUL-1999) Makino Sou-ichi, Obihiro University of Agriculture and Veterinary Medicine, Department of Veterinary Microbiology, Inada, Obihiro, Hokkaido 080-8555, Japan (E-mail:smakino@obihiro.ac.jp, URL: http://www.obihiro.ac.jp, Tel: 81-155-49-5386, Fax: 81-155-49-5402)  
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Best Local Similarity 99.4%; Pred. No. 1,2e-251;  
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DB 61 GTTGCGAAGGAATTTACCTTGAAGCTTCTGACATGCAAGACGATGATGATTTGCTGAAT 120  
QY 163 GTCATTCGCTCTGCAATAGGTAAGTCTCATACAGACTATTTTCATCAGAGGTAAGCTCTTTA 222  
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QY 223 CTGATGATGATAGTGGCACAAGGATTAATTTGTTTGCAGTTGATGTCACAGAGGATGAT 282  
DB 181 CTGATGATGATAGTGGCACAAGGATTAATTTGTTTGCAGTTGATGTCACAGAGGATGAT 240  
QY 283 CCAAGAGAGGGGGCTTAAATCTACGGCTTATGTTGCAAGAAATTTATATGTC 342  
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DB 481 TATCTGATTTAATGTCGATAGTGAACCTGACGACGAGTGTGCAAGCGATG 540  
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DB 541 TTACGGTTTGTATCTGACAGCTGAAAGCTTACGTTTGGCAATACAGAGGGATTT 600  
QY 643 CGTCAACACATGATGATCTCAGTGGCGTTCTTATGATATGATGCTGGAAGTGTGAT 702  
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DB 661 CTTCATTTGAACCTGGGGAAGGTTAGTAGCGTCTGCTGACATCATGACAAAGCTCT 720  
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DB 841 TCTATGTCGCGGAGATGAGAGTCCGTGGGATTAAGCACAATTAATTTGTTGGAT 900  
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RESULT 13  
LOCUS SSO132761 1362 bp DNA linear BCT 09-OCT-2000  
DEFINITION Shigella sonnei stx1 and stx2 genes.

ACCESSION AJ132761  
 VERSION AJ132761.1 GI:4454334  
 KEYWORDS stx<sub>2</sub> gene; Stx<sub>2</sub> protein; stx<sub>2</sub> gene; Stx<sub>2</sub> protein.  
 SOURCE Shigella sonnei  
 ORGANISM Shigella sonnei  
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.  
 REFERENCE 1  
 AUTHORS Beutin, L., Strauch, E. and Fischer, I.  
 TITLE Isolation of Shigella sonnei lyogenic for a bacteriophage encoding gene for production of Shiga toxin  
 JOURNAL Lancet 353 (9163), 1498 (1999)  
 PUBMED 10232325  
 REFERENCE 2 (bases 1 to 1362)  
 AUTHORS Beutin, L.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-FEB-1999) Beutin L., Emerging Bacterial Pathogens, Robert Koch Institut, Nordufer 20, D-13353 Berlin, GERMANY  
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 Query Match 58.3%; Score 879; DB 15; Length 1362;  
 Best Local Similarity 99.4%; Pred. No. 1,2e-251;  
 Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 283 CCAGAGGAGGCGGTTTAATATCTACGGCTTATTTGTGAACGAATATTAATATATG 342  
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 334 CCAGAGGAGGCGGTTTAATATCTACGGCTTATTTGTGAACGAATATTAATATG 393  
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 394 ACAGATTTGTTTACAGACAAATATATGTTTATTCGCTTTCGATTTTCAATGTT 453  
 QY 403 ACCCTTCAGGTACAAACAGCGGTTACATTGTCGTGTGACAGTATATACACGTTACG 462  
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 454 ACCCTTCAGGTACAAACAGCGGTTACATTGTCGTGTGACAGTATATACACGTTACG 513  
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 574 TATCTGATTTATATGTCGATATGTTGAACCTCAGACGAGCTGTGTGCAAGACGATG 633  
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 QY 703 CTATCATGAACTGAGGAGGAGGTTGAGTACCGCTGCTGCTGATCATGAGACGATCT 762  
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 754 CTATCATGAACTGAGGAGGAGGTTGAGTACCGCTGCTGCTGATCATGAGACGATCT 813  
 QY 763 GTTCGTGTGAGAAATTTCTTTGGAAGCATTAATGCAATTCGGAACGCTGATTA 822  
 DB |||||  
 814 GTTCGTGTGAGAAATTTCTTTGGAAGCATTAATGCAATTCGGAACGCTGATTA 873  
 QY 823 ATACGAAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 882  
 DB |||||  
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 QY 883 TCTATGTCGCGGACAGATGAGAGAGTCCGTGGATTAACGACAAATTAATTTGGAGAT 942  
 DB |||||  
 934 TCTATGTCGCGGACAGATGAGAGAGTCCGTGGATTAACGACAAATTAATTTGGAGAT 993  
 QY 943 TCATCCACTCTGCGGCAATTCGATGCGCAGACATTAATGACGATGG 989  
 DB |||||  
 994 TCATCCACTCTGCGGCAATTCGATGCGCAGACATTAATGACGATGG 1040  
 RESULT 14  
 SHFSHT 1500 bp DNA linear BCT 21-APR-1996  
 LOCUS S.dysenteriae type 1 Shiga toxin alpha and beta subunit (stx<sub>2</sub> and  
 DEFINITION stx<sub>2</sub> genes, complete cds.  
 ACCESSION M19437.1 GI:152784  
 VERSION M19437.1  
 KEYWORDS Shiga toxin.  
 SOURCE Shigella dysenteriae  
 ORGANISM Shigella dysenteriae  
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.  
 REFERENCE 1 (bases 1 to 1500)  
 AUTHORS Stroockbine, N.A., Jackson, M.P., Sung, L.M., Holmes, R.K. and O'Brien, A.D.  
 TITLE Cloning and sequencing of the genes for Shiga toxin from Shigella  
 JOURNAL J. Bacteriol. 170 (3), 1116-1122 (1988)  
 PUBMED 2830229  
 COMMENT Original source text: Shigella dysenteriae (clone: pNBS13.) DNA.  
 Draft entry and computer-readable sequence for [1] kindly provided by M.Jackson, 02-JUN-1988.  
 FEATURES  
 Location/Qualifiers

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CDS	161..1108	
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ORIGIN	726 bp upstream of HindIII site.	
Query Match	58.3%; Score 879; DB 15; Length 1500;	
Best Local Similarity	99.4%; Pred. No. 1.1e-251;	
Matches	882; Conservative 0; Mismatches 5; Indels 0; Gaps 0,	
OY	103 GATCTGAAGAATTTCACCTTAGACTTCTCGACTCGCAAGACGTATGTAGATTCCGCTGAAT	162
DB		
DB	221 GTTGCGAAGAAATTACCCTTAGACTCTTCGACTGCMAAGACCTAAGTAGATTCCGCTGAAT	280
OY	163 GTCATTGCGCTCGCAATAGTGATCTCCATTACAGACTATTTTCATCGAGAGTACGCTCTTAA	222
DB	281 GTCATTCCTCTGCAATAGTACTCATTACACACTATTTTCATCGAGAGTACGCTCTTAA	340
OY	223 CTGATGATTGATGTGGCACAGGGGATAATTTGTTTGCAGTTGATGTCAAGAGGATTAAT	282
DB	341 CTGATGATTGATGTGGCACAGGGGATTAATTTGTTTGCAGTTGATGTCAAGAGGATTAAT	400
OY	283 CCAGAGGAAGCGCGTTTAATPATCTACGGCTATTTGTGAACGAAATTAATTTAATATG	342
DB	401 CCAGAGGAAGCGCGTTTAATPATCTACGGCTATTTGTGAACGAAATTAATTTAATATG	460
OY	343 ACAGAGTTTGTTAACAGACAATATGTTTTTATCGCTTGCTGATTTTTCACATGTT	402
DB	461 ACAGAGTTTGTTAACAGACAATATGTTTTTATCGCTTGCTGATTTTTCACATGTT	520
OY	403 ACCTTTCCAGGTACAAACAGCGGTACATTGCTGGTGACAGTACGATTAACACGTTACAG	462
DB	521 ACCTTTCCAGGTACAAACAGCGGTACATTGCTGGTGACAGTACGATTAACACGTTACAG	580

OY		463	CGGTTCACAGGAATCAATCGAAGGGGATGCAGATAAATGCCATTGCTTGACTACTACTTCT	522
Db		581	CGTTTCACAGGAATCAGTCGTAAGGGGATGCAGATAAATGCCATTGCTTGACTACTACTTCT	640
OY		523	TATCTGATTTAAATGTGCGCATAGTGAACCTCACTGAACGAGTCTGTGGCAAGCCATG	582
Db		641	TATCTGATTTAAATGTGCGCATAGTGAACCTCACTGAACGAGTCTGTGGCAAGCCATG	700
OY		583	TTACGGTTTTGTACTGTGACAGCTGAAGCTTTACGTTTGGCAAATACAGAGGGGATTT	642
Db		701	TTACGGTTTTGTACTGTGACAGCTGAAGCTTTACGTTTGGCAAATACAGAGGGGATTT	760
OY		643	CGTACAACACCTGAGTAGATCTCAGTGGGCGTTCCTATGTAAATGACTGTGGAAGTGTGAT	702
Db		761	CGTACAACACCTGAGTAGATCTCAGTGGGCGTTCCTATGTAAATGACTGTGGAAGTGTGAT	820
OY		703	CTTACATTGAACCTGGGGAAGGTGAGTGAAGCGTCTGCTGACTATCATGCAAGAAGCTCT	762
Db		821	CTTACATTGAACCTGGGGAAGGTGAGTGAAGCGTCTGCTGACTATCATGCAAGAAGCTCT	880
OY		763	GTTGCGTAGGAAGAAATTTCTTTTGGAAAGCATTTATGCAATTTCTGGGAAGCGTGGCAATTA	822
Db		881	GTTGCGTAGGAAGAAATTTCTTTTGGAAAGCATTTATGCAATTTCTGGGAAGCGTGGCAATTA	940
OY		823	ATACTGAATTTGTCATCATATGATCATTCGAGATTGCCAGATGSCATCTGATGATTTCTT	882
Db		941	ATACTGAATTTGTCATCATATGATCATTCGAGATTGCCAGATGSCATCTGATGATTTCTT	1000
OY		883	TCTATGTGTCGGGAGATGGAAGAGTCGCTGGGATTTACGCCAATPAATAATTTGTGGGAT	942
Db		1001	TCTATGTGTCGGGAGATGGAAGAGTCGCTGGGATTTACGCCAATPAATAATTTGTGGGAT	1060
OY		943	TCATCCACTCTGGGGGCGCAATTCGTATGCGCGAAGCTATTAGCAGTGG	989
Db		1061	TCATCCACTCTGGGGGCGCAATTCGTATGCGCGAAGCTATTAGCAGTGG	1107
RESULT 15				
AF461172				
LOCUS				
DEFINITION			1956 bp DNA linear BCT 01-JUL-2002	
			Escherichia coli PDJ30 Shiga toxin 1A subunit (stx1A) and Shiga	
			toxin 1B subunit (stxB) genes, complete cds.	
ACCESSION			AF461172	
VERSION			AF461172.1	
KEYWORDS			GI:21636532	
SOURCE				
ORGANISM			Escherichia coli	
			Escherichia coli	
			Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
			Enterobacteriaceae; Escherichia.	
REFERENCE			1 (bases 1 to 1956)	
AUTHORS			Yu,J.Y., Jeon,H.G., Kang,Y.H., Kim,E.C., Sohn,C.K. and Lee,B.K.	
TITLE			Characterization of Shiga toxin genes in Shiga toxin-producing	
JOURNAL			Escherichia coli isolated in Korea	
FEATURES			Unpublished	
source			2 (bases 1 to 1956)	
REFERENCE			1. 1956	
AUTHORS			Yu,J.Y., Jeon,H.G., Kang,Y.H., Kim,E.C., Sohn,C.K. and Lee,B.K.	
TITLE			Direct Submission	
JOURNAL			Submitted (19-Dec-2001) Dept. of Microbiology, National Institute	
			of Health, Korea, 5 Noksong-dong Eunpyong-gu, Seoul 122-701, Korea	
			Location/Qualifiers	
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/translation="MKKTLIASLSFFSASALATPDVTKVEYTKYNDDETIVKV
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Query Match 58.3%; Score 879; DB 15; Length 1956;

Best Local Similarity 99.4%; Pred. No. 1.1e-251;

Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 103 GATCTGAAGAATTACTTACTAGACTCTGCTGCAAGACGATGATGATGATGATGAT 162
DB 748 GTTGCAGAGAAATTACTTACTAGACTCTGCTGCAAGACGATGATGATGATGAT 807
QY 163 GTCAATTCGCTCTGCAATAGGTAAGTCTCAATTAACAATTTTCATCAGAGGTAAGTCTTTA 222
DB 808 GTCAATTCGCTCTGCAATAGGTAAGTCTCAATTAACAATTTTCATCAGAGGTAAGTCTTTA 867
QY 223 CTGATGATTTATGATGCAACAGAGGAAATTTGTTGCACTGATGATGATGATGATGAT 282
DB 868 CTGATGATTTATGATGCAACAGAGGAAATTTGTTGCACTGATGATGATGATGATGAT 927
QY 283 CCAGAGAGAGGCGGTTAATTAATCTACGGCTTAATGTTGACGAAATAATTTATATG 342
DB 928 CCAGAGAGAGGCGGTTAATTAATCTACGGCTTAATGTTGACGAAATAATTTATATG 987
QY 343 ACAGGATTTGTTAACAAGCAATTAATGTTTATGCTTGTGCTGATTTTTCATGTT 402
DB 988 ACAGGATTTGTTAACAAGCAATTAATGTTTATGCTTGTGCTGATTTTTCATGTT 1047
QY 403 ACCGTTCCAGGTCAACAGAGGTTACATGCTGCTGAGACAGTACGCTATACAGCTTACAG 462
DB 1048 ACCGTTCCAGGTCAACAGAGGTTACATGCTGCTGAGACAGTACGCTATACAGCTTACAG 1107
QY 463 CGTGTTCAGAGGATCAGTCTGACGGGATGACAGTAATGCGCAATTCGTTGACTACTTCT 522
DB 1108 CGTGTTCAGAGGATCAGTCTGACGGGATGACAGTAATGCGCAATTCGTTGACTACTTCT 1167
QY 523 TATCTGATTTAATGTCATAGTGAACCTCACTGACGAGTCTGTGCAAGAGCGATG 582
DB 1168 TATCTGATTTAATGTCATAGTGAACCTCACTGACGAGTCTGTGCAAGAGCGATG 1227
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DB 1228 TTACGTTGTTTACGACAGCTGAAGCTTTACGTTTGGCAAAATACAGAGGGGATTT 1287
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DB 1348 CTTTCAATTGAACGAGGAAAGTTAGTAGGCTCTGCTGATCACTATGACAAAGACTCT 1407
QY 763 GTTGTGTAGAGAAATTTCTTTTGAAGACATTAATGCAATTCGGAAGCGTGGCATTA 822
DB 1408 GTTGTGTAGAGAAATTTCTTTTGAAGACATTAATGCAATTCGGAAGCGTGGCATTA 1467

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QY 823 ATACTGAATTGTCATCATCATGATCGGAGTTGCCAGAAATGCGATGATGATTTTCT 882
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DB 1528 TCTATGTTCCGGGAGATGAGAAAGTCCGTGGGATTAACGCAATTAATAATTTGGGAT 1587
QY 943 TCATCCACTCTGGGGCAATTCTGATGCGCAGAACTATTACAGTGG 989
DB 1588 TCATCCACTCTGGGGCAATTCTGATGCGCAGAACTATTACAGTGG 1634

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Search completed: January 23, 2007, 04:04:22  
Job time : 8801 secs

PT Bacterial cell for recombinantly expressing bacterial toxins in large quantities useful for immunization and treatment of bacterial infections  
PT comprises expression vector encoding bacterial toxin.

XX Example 7; Col 129-134; 83bp; English.  
 CC E. coli verotoxin (VT) types 1 and 2 subunit A were cloned into pMal-p2,  
 CC designed to allow expression of the native proteins as C-terminal fusions  
 CC to a periplasmically-secreted version of maltose binding protein (MBP).  
 CC VT B chains are small proteins (approximately 8 kDa), so use of a small  
 CC affinity tag was preferred (i.e. polyhistidine). A polyhistidine affinity  
 CC tag facilitates single step affinity purification of subunits from  
 CC periplasmic extracts. However, due to poor recovery of his-tagged VT-1 A  
 CC and VT-2 A chains, expression of MBP fused subunits was undertaken. Due  
 CC to the toxicity of the VT-2 B subunit, strict uninduced promoter control  
 CC is necessary to permit cell viability. Bacterial host cells expressing a  
 CC recombinant expression vector encoding a polyhistidine affinity tag and a  
 CC portion of the VT-2 B chain are claimed. The vector is chosen from  
 CC pET24hisVT2BL+, pET24hisVT2BL- and pET24VT2B, where "L+" indicates that  
 CC the vector encodes the preprotein form of the protein and "L-" indicates  
 CC that the vector encodes the mature form of the protein. The bacterial  
 CC cell is capable of expressing large quantities (40 mg/l) of VT-2B. The  
 CC toxins are useful for immunizing non-mammals and for detecting bacterial  
 CC toxins in environmental samples including soil, water, industrial  
 CC samples, biological samples and samples obtained from food and dairy  
 CC processing instruments

XX Sequence 2073 BP; 578 A; 448 C; 535 G; 512 T; 0 U; 0 Other;

Query Match 58.5%; Score 881.4; DB 3; Length 2073;

Best Local Similarity 99.3%; Pred. No. 1.2e-253;

Matches 885; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 99 CCCGAGTCTGAGAGAAATTTACCTTACCTTCTGACTGCAAGAACGTATGTAGATTGCGT 158  
 DB 1182 CCCGGAATTCAGAGAAATTTACCTTACCTTCTGACTGCAAGAACGTATGTAGATTGCGT 1241  
 QY 159 GAATGTCATTCGCTCTGTCATAGGTAAGTCTCATTCACAGCTATTTTCATCAGAGATGTC 218  
 DB 1242 GAATGTCATTCGCTCTGTCATAGGTAAGTCTCATTCACAGCTATTTTCATCAGAGATGTC 1301  
 QY 219 TTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 278  
 DB 1302 TTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1361  
 QY 279 AGATCCAG 338  
 DB 1362 AGATCCAG 1421  
 QY 339 TGTGACAGAGATTTGTTAAACAGACAAATTAATGTTTATGCGTTGCGATTTTTCACA 398  
 DB 1422 TGTGACAGAGATTTGTTAAACAGACAAATTAATGTTTATGCGTTGCGATTTTTCACA 1481  
 QY 399 TGTACTCTTCCAGAGTACACAGAGGTTTACATTTGCTGTGACAGTATACCAAGTT 458  
 DB 1482 TGTACTCTTCCAGAGTACACAGAGGTTTACATTTGCTGTGACAGTATACCAAGTT 1541  
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 DB 1602 TTCTTATCTGAGATTTATGTCGATGTGACAGTCTGACAGAGTCTGTGCAAGAGC 1661  
 QY 579 GATGTTACGCTTTGTTATCTGTGACAGCTGAAGCTTTTACGTTTCCGCAATTAACAGAGGG 638  
 DB 1662 GATGTTACGCTTTGTTATCTGTGACAGCTGAAGCTTTTACGTTTCCGCAATTAACAGAGGG 1721  
 QY 639 ATTTTGTACAACTGATGATCTCAGTGGCGTTCTTATGTTATGATGCTGCAAGATGT 698  
 DB 1722 ATTTTGTACAACTGATGATCTCAGTGGCGTTCTTATGTTATGATGCTGCAAGATGT 1781  
 QY 699 TGAATTTACATTTGAATCGGGAGAGGTTGAGTACGCTGCTGCAATCATGATGAGACAGA 758  
 DB 1782 TGAATTTACATTTGAATCGGGAGAGGTTGAGTACGCTGCTGCAATCATGATGAGACAGA 1841

QY 759 CTCTGTGCTGTGAGAGAAATTTCTTTTGAAGCATTAATGCAATTTCTGGAGCGTGGC 818  
 DB 1842 CTCTGTGCTGTGAGAGAAATTTCTTTTGAAGCATTAATGCAATTTCTGGAGCGTGGC 1901  
 QY 819 ATTAATGATGAAATTTGTCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 878  
 DB 1902 ATTAATGATGAAATTTGTCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1961  
 QY 879 TCCTCTATGTCCTGGGAGATGAGAGATGCGTGGAGTTACGCAATTAATTAATTTGTG 938  
 DB 1962 TCCTCTATGTCCTGGGAGATGAGAGATGCGTGGAGTTACGCAATTAATTAATTTGTG 2021  
 QY 939 GGATTCATCATCTCTGGGAGCAATTTCTGATGCGCAGAACTATTACAGATGG 989  
 DB 2022 GGATTCATCATCTCTGGGAGCAATTTCTGATGCGCAGAACTATTACAGATGG 2072

RESULT 2  
 ID ABRK11957  
 ABK11957 standard; cDNA; 2073 BP.  
 XX  
 AC ABRK11957;  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE cDNA encoding MBP-VT1-A fusion protein #2.  
 XX  
 KW Verotoxin; antitoxin; antidiarrheal; antibacterial; haemostatic; vaccine;  
 KW haemorrhagic cystitis; dalmanitis; MBP-VT1-A; haemolytic uremic syndrome;  
 KW thrombotic thrombocytopenic purpura; ss.  
 XX  
 OS Escherichia coli.  
 XX  
 FT Key  
 FT CDS Location/Qualifiers  
 FT 1..2073  
 FT /\*tag= a  
 FT /product= "MBP-VT1-A fusion protein #2"  
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 PN US2002012656-A1.  
 XX  
 PD 31-JUN-2002.  
 XX  
 PF 16-JUN-1999; 99US-00334477.  
 XX  
 PR 13-MAR-1997; 97US-00816977.  
 XX  
 PA (WILL/) WILLIAMS J A.  
 PA (BYRN/) BYRNE L M.  
 PA (PUGH/) PUGH C S G.  
 XX  
 PI Williams JA, Byrne LM, Pugh CSG;  
 XX  
 DR WPI; 2002-205094/26.  
 DR P-PSDB; AA077830.  
 XX  
 PT New recombinant expression vector encoding affinity tag and Escherichia  
 PT coli type 1 or type 2 verotoxin, useful for treating or preventing  
 PT diseases due to E. coli verotoxins and in producing vaccines.  
 XX  
 PS Example 7; Page 69-71; 98bp; English.  
 XX  
 CC This invention relates to a recombinant expression vector encoding an  
 CC affinity tag and protein comprising at least a portion of a bacterial  
 CC toxin consisting of Escherichia coli type 1 or type 2 verotoxin. The  
 CC expression vector can be used to produce recombinant verotoxin protein  
 CC which can be used to create a vaccine against diseases caused by E. coli  
 CC such as verotoxin haemorrhagic cystitis and dalmanitis. The antitoxins  
 CC are useful for treating humans and animals intoxicated with a bacterial  
 CC toxin, particularly E. coli verotoxin. The antitoxins may also be used in  
 CC the preventative treatment and in diagnostic assays to detect the  
 CC presence of a toxin in a sample. The polypeptides derived from E. coli

CC verotoxins are useful as immunogens for the production of vaccines,  
 CC including multivalent vaccines and antitoxins, which can be administered  
 CC to a subject at risk of diarrhoeal disease or at risk of developing extra  
 CC -intestinal complications of E. coli infections, e.g. haemolytic uremic  
 CC syndrome, thrombotic thrombocytopenic purpura. The present sequence  
 CC represents the cDNA encoding the MBPvtx1-A protein #2 of the invention.  
 CC This fusion protein was created to facilitate purification of the  
 CC recombinant proteins of the invention  
 CC  
 XX

Sequence 2073 BP, 578 A, 448 C, 535 G, 512 T, 0 U, 0 Other;

Query Match 58.5%; Score 881.4; DB 6; Length 2073;

Best Local Similarity 99.3%; Pred. No. 1.2e-253;

Matches 885; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

QY 99 CCCAGATCTGAAGAAATTACCTTAGACTTCTCGACTGCAAGACGATATGATGGCT 158
DB 1182 CCCGGAATTCAAGAAATTACCTTAGACTTCTCGACTGCAAGACGATATGATGGCT 1241
QY 159 GAATGTCATTCGCTCTGCAATAGGACTCCATTCACAGACTTTTCATCAGAGGATGCT 218
DB 1242 GAATGTCATTCGCTCTGCAATAGGACTCCATTCACAGACTTTTCATCAGAGGATGCT 1301
QY 219 TTTTACTGATGATGATAGTACGACAGAGGATATTTTTCAGTTGATGATGATGAT 278
DB 1302 TTTTACTGATGATGATAGTACGACAGAGGATATTTTTCAGTTGATGATGATGAT 1361
QY 279 AGATTCAGAGAGAGAGGCGGTTTAAATATCTACGCTTATTTGTAAGCAAAATATTTATA 338
DB 1362 AGATTCAGAGAGAGAGGCGGTTTAAATATCTACGCTTATTTGTAAGCAAAATATTTATA 1421
QY 339 TGTGACAGAGATTTGTAACAGACAAATATGTTTATGCTGCTTGTGATTTTTCACA 398
DB 1422 TGTGACAGAGATTTGTAACAGACAAATATGTTTATGCTGCTTGTGATTTTTCACA 1481
QY 399 TGTTACCTTTCCAGGTACACAGCGGTTACATTTGTTGTGACAGTACCTATACACGCTT 458
DB 1482 TGTTACCTTTCCAGGTACACAGCGGTTACATTTGTTGTGACAGTACCTATACACGCTT 1541
QY 459 ACAGGCTTTCAGAGGATACAGCTGACAGGAGATGAGATTAATGCGCCATTTGTTGACTAC 518
DB 1542 ACAGGCTTTCAGAGGATACAGCTGACAGGAGATGAGATTAATGCGCCATTTGTTGACTAC 1601
QY 519 TTTCTATCTGATTTAAATGTCGATAGTGAACCTCAGTGAAGAGTGTGAGCAAGAGC 578
DB 1602 TTTCTATCTGATTTAAATGTCGATAGTGAACCTCAGTGAAGAGTGTGAGCAAGAGC 1661
QY 579 GATGTTACGGTTTGTACTGTGACAGCTGAAGCTTTACGTTTCGGCAAAATACAGAGGG 638
DB 1662 GATGTTACGGTTTGTACTGTGACAGCTGAAGCTTTACGTTTCGGCAAAATACAGAGGG 1721
QY 639 ATTTGGTCAACACCTGATGATCTCAGTGGGCGTTCTTATGTAATGACTGCTGAAGATGT 698
DB 1722 ATTTGGTCAACACCTGATGATCTCAGTGGGCGTTCTTATGTAATGACTGCTGAAGATGT 1781
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DB 1962 TCTCTTATGTTGTCGGGAGATGAGAGACTCGTGGGATTTAGCACAATTAATAATTTGTG 2021
QY 939 GGATTCATCACTCTGGGGGCAATTTGTGATGCGCAGAACTATTAGCAGTGG 989
DB 989 GGATTCATCACTCTGGGGGCAATTTGTGATGCGCAGAACTATTAGCAGTGG 989

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DB 2022 GGATTCATCACTCTGGGGGCAATTTGTGATGCGCAGAACTATTAGCAGTGG 2072

RESULT 3

AA227687  
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AA227687;

22-DEC-1999 (first entry)

Verotoxin 1 gene.

Verotoxin; VT1, VT2; detection; PCR primer; ss.

Escherichia coli.

JPL1243996-A.

14-SEP-1999.

27-FEB-1998; 98UP-00047677.

27-FEB-1998; 98UP-00047677.

(TOYM ) TOYOBO KK.

WP1; 1999-603716/52.

An oligonucleotide for amplification of verotoxin - useful in the detection of inactivated verotoxin gene by transfer of a foreign DNA fragment.

Claim 1; Page 8; 10pp; Japanese.

This sequence represents the Escherichia coli verotoxin1 (VT1) gene. The invention relates to an oligonucleotide for amplification of VT. The oligonucleotide is useful for detection of inactivated VT gene by transfer of a foreign DNA fragment. Simple, rapid and specific amplification of VT gene from environmental factors is achieved using the oligonucleotide of the invention

Sequence 1369 BP, 379 A, 225 C, 330 G, 435 T, 0 U, 0 Other;

Query Match 58.4%; Score 880.4; DB 2; Length 1369;

Best Local Similarity 99.9%; Pred. No. 1.8e-253;

Matches 881; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 108 GAAGGAATTTACCTTAACTTCTGACTGCAAGACGATATGATTCGCTGAATGTCAT 167
DB 98 GAAGGAATTTACCTTAACTTCTGACTGCAAGACGATATGATTCGCTGAATGTCAT 157
QY 168 TCGCTGCAATAGTACTCCATTCACAGACTATTTTCATCAGAGGATAGCTTTACTGAT 227
DB 158 TCGCTGCAATAGTACTCCATTCACAGACTATTTTCATCAGAGGATAGCTTTACTGAT 217
QY 228 GATTGATAGTGGCAACAGGGATTAATTTGTCAGTTGATGTCAGAGGATAGTCCAGA 287
DB 218 GATTGATAGTGGCAACAGGGATTAATTTGTCAGTTGATGTCAGAGGATAGTCCAGA 277
QY 288 GGAAGGGCGGTTTAAATATCTACAGGCTTATGTTGAAGCAATTAATTAATGAGACAG 347
DB 278 GGAAGGGCGGTTTAAATATCTACAGGCTTATGTTGAAGCAATTAATTAATGAGACAG 337
QY 348 ATTTGTTACAGAGCAAAATATGTTTATCGCTTGTGCTGATTTTTCACATGTTACTCT 407
DB 338 ATTTGTTACAGAGCAAAATATGTTTATCGCTTGTGCTGATTTTTCACATGTTACTCT 397
QY 408 TCCAGGTACCAACAGGGTTACATTTGCTGTGACAGTACGATATACAGGTTACAGCGTGT 467
DB 398 TCCAGGTACCAACAGGGTTACATTTGCTGTGACAGTACGATATACAGGTTACAGCGTGT 457
QY 468 TGCAGGATCACTGCTACAGGGGATGACAGATTAATGCGCAATTCGTTGACTTCTTATCT 527
DB 457 TGCAGGATCACTGCTACAGGGGATGACAGATTAATGCGCAATTCGTTGACTTCTTATCT 527

```



Db	458	TCGACGAGATCAGTCCGACGGGGATGAGATGAATTCGCCATTCGTTGACTCACTTATCT	517
Oy	528	GGATTTAATGTCGCATATGTGAACTTCACTGACGCACTGTGTGGCAAGCCGATGTTACG	587
Db	518	GGATTTAATGTCGCATATGTGAACTTCACTGACGCACTGTGTGGCAAGCCGATGTTACG	577
Oy	588	GTTTGTACTGTGACAGCTGAAGCTTTACGTTTTCGGCAAAATACAGAGGGGATTTGCTAC	647
Db	578	GTTTGTACTGTGACAGCTGAAGCTTTACGTTTTCGGCAAAATACAGAGGGGATTTGCTAC	637
Oy	648	AACTGATGATGATCTTCAGTGGGCGTTCTAATGTAATGACTGCTGAAGATGTGATCTTAC	707
Db	638	AACTGATGATGATCTTCAGTGGGCGTTCTAATGTAATGACTGCTGAAGATGTGATCTTAC	697
Oy	708	ATTGAATCTGGGAAAGGTTGAGTAGCGTCCCTGCTGACTATCATGAGCAAAACTCTGTTCG	767
Db	698	ATTGAATCTGGGAAAGGTTGAGTAGCGTCCCTGCTGACTATCATGAGCAAAACTCTGTTCG	757
Oy	768	TGTAGGAAGAATTTCTTTTGGAAAGCATTAATGCAATTCCTGGAAAGCTGCAATTAATCT	827
Db	758	TGTAGGAAGAATTTCTTTTGGAAAGCATTAATGCAATTCCTGGAAAGCTGCAATTAATCT	817
Oy	828	GAAATGTCATCATCATGATGATCGCGAGTTGCCAGAAATGSCATCTGATGAGTTCCCTCTAT	887
Db	818	GAAATGTCATCATCATGATGATCGCGAGTTGCCAGAAATGSCATCTGATGAGTTCCCTCTAT	877
Oy	888	GGTCCGCGAGATGGAAGAGTCCGTGGGATTAAGCAATTAATATGTGGGATTCATC	947
Db	878	GGTCCGCGAGATGGAAGAGTCCGTGGGATTAAGCAATTAATATGTGGGATTCATC	937
Oy	948	CACCTCTGGGGGCAATTCGATGTCGCGAGAACTTATTAAGCAGTTG	989
Db	938	CACCTCTGGGGGCAATTCGATGTCGCGAGAACTTATTAAGCAGTTG	979

RESULT 4

ADL25576

ID ADL25576 standard; DNA; 1227 BP.

AC ADL25576;

XX

DT 20-MAY-2004 (first entry)

XX

DE S. dysenteriae shiga toxin gene stx-dysenteriae.

XX

KM Shiga toxin; ds: gene; fluorescence resonance energy transfer; FRET;

XX

KM gastrointestinal disease; dysentery.

XX

OS Shigella dysenteriae.

XX

PN US2003215814-A1.

XX

PD 20-NOV-2003.

XX

PF 17-MAY-2002; 2002US-00150792.

XX

PR 17-MAY-2002; 2002US-00150792.

XX

PA (COCK/) COCKERILL F R.

PA (ROSE/) ROSENBLATT J E.

PA (SLOA/) SLOAN L.

PA (UHLJ/) UHL J R.

XX

PI Cockerill FR, Rosenblatt JE, Sloan L, Uhl JR;

XX

DR WPI; 2003-902026/82.

XX

PT Detecting presence or absence of Shiga toxin producing organisms in

PT biological sample, by amplifying nucleic acid encoding Shiga toxin with

PT pair of stx1 primers and detecting fluorescence resonance energy

PT transfer.

XX

Example2.Fig 1; 24bp; English.

xx The invention relates to detecting the presence or absence of Shiga toxin  
cc or Shiga-like toxin producing organisms in a biological sample involving  
cc amplifying nucleic acid encoding Shiga toxin with a pair of stx1 primers,  
cc detecting the amplified product with labelled stx1 probes, and detecting  
cc the presence or absence of fluorescence resonance energy transfer (FRET).  
cc Also included is an article of manufacture comprising the stx1 primers  
cc and probes and a donor fluorescent moiety and corresponding fluorescent  
cc moiety or a pair of stx2 primers, a pair of stx2 probes and a donor  
cc fluorescent moiety and corresponding fluorescent moiety. The method is  
cc useful for detecting the presence or absence of one or more Shiga toxin  
cc or Shiga-like toxin producing organism e.g. *Escherichia coli* (especially  
cc gastrointestinal disease causing strains) and *Shigella* (causative agent  
cc of dysentery) in a biological sample which is a stool sample or body  
cc fluids from an individual. The method which is rapid and specific in detecting  
cc the Shiga toxin from biological samples. The present sequence is a  
cc bacterial Shiga toxin or shiga-like toxin gene used to design the primers  
cc and probes of the invention.  
cc  
cc  
cc  
xx

Sequence 1227 BP; 334 A; 204 C; 298 G; 389 T; 0 U; 2 Other;

Query Match	58.4%	Score 879.6;	DB 11;	Length 1227;
Best Local Similarity	99.7%;	Pred. No. 3e-253;		
Matches 879;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0
108 GAAGGAATTTACCTTAGACTTCTCCACTGCAAGACGATATGATATTCGCTGAATGTCAT				167
66 GAAGGAATTTACCTTAGACTTCTCCACTGCAAGACGATATGATATTCGCTGAATGTCAT				125
168 TCGCTCTGCATATAGTACTTCCATTACAGACTATTTTCATCAGAGGTAAGCTCTTACTGAT				227
126 TCGCTCTGCATATAGTACTTCCATTACAGACTATTTTCATCAGAGGTAAGCTCTTACTGAT				185
228 GATTGATATGTGGCACAAGGGAATTAATTTGTTTGCAGTTATATGCAAGAGGATAGATCCAA				287
186 GATTGATATGTGGCACAAGGGAATTAATTTGTTTGCAGTTATATGCAAGAGGATAGATCCAA				245
288 GGAAGGCGGCTTTAATTAATCTACGGCTTATGTTGAAGAAATTAATTATATGTGCAGG				347
246 GGAAGGCGGCTTTAATTAATCTACGGCTTATGTTGAAGAAATTAATTATATGTGCAGG				305
348 ATTGTTTAAACGAGCAAAATTAATGTTTTTATGCTTGGCTGATTTTTTACATGTAACCTT				407
306 ATTGTTTAAACGAGCAAAATTAATGTTTTTATGCTTGGCTGATTTTTTACATGTAACCTT				365
408 TCCAGGTACAAACAGCGGTTTACATTTCTCTGTGACAGTAGACTATACCACGTTACAGCGGT				467
366 TCCAGGTACAAACAGCGGTTTACATTTCTCTGTGACAGTAGACTATACCACGTTACAGCGGT				425
468 TGCAGGATCAAGTCGTAACGGGATGACAGATAAATGGCCATTCGTTGACATACTTCTATCT				527
426 TGCAGGATCAAGTCGTAACGGGATGACAGATAAATGGCCATTCGTTGACATACTTCTATCT				485
528 GGATTTAATGTGCGAATAGTGAACCTCACTGACGAGCTGTGTGGCAAGAGCATGTTACG				587
466 GGATTTAATGTGCGAATAGTGAACCTCACTGACGAGCTGTGTGGCAAGAGCATGTTACG				545
588 GTTTGTTACTGTGACAGCTGAAGCTTTTACGTTTTTGGCAAAATACAGAGGGGATTTGTAAC				647
546 GTTTGTTACTGTGACAGCTGAAGCTTTTACGTTTTTGGCAAAATACAGAGGGGATTTGTAAC				605
648 AACACTGATGATCTCAGTGGGCGTTCTTAATGATATGATGCGGAAGATGTTGATCTTAC				707
606 AACACTGATGATCTCAGTGGGCGTTCTTAATGATATGATGCGGAAGATGTTGATCTTAC				665
708 ATTGAATCGGGGAAGGTTAGTAGGCGTCTGCTGACATAATCATGACCAAGACTCTGTTCG				767
666 ATTGAATCGGGGAAGGTTAGTAGGCGTCTGCTGACATAATCATGACCAAGACTCTGTTCG				725
768 TGTAGGAAGAAATTTCTTTTGGAGAATTAATGCAATTCGAGGAAGCGGTGGCAATTAATCT				827
726 TGTAGGAAGAAATTTCTTTTGGAGAATTAATGCAATTCGAGGAAGCGGTGGCAATTAATCT				785

QY 828 GAATGTCATCATCATGATCGGAGTTCGCGAATGCGATCTGATGAGTTTCCTCAT 887  
 DB 786 GAATGTCATCATCATGATCGGAGTTCGCGAATGCGATCTGATGAGTTTCCTCAT 845  
 QY 888 GTGTCGGGAGATGAGAGAGTCCGTGGGATTACGACATATAATATTTGGGATTCTATC 947  
 DB 846 GTGTCGGGAGATGAGAGAGTCCGTGGGATTACGACATATAATATTTGGGATTCTATC 905  
 QY 948 CACTCTGGGGGCAATTTCTGATGCGGAGAACTATTAGCAGTGG 989  
 DB 906 CACTCTGGGGGCAATTTCTGATGCGGAGAACTATTAGCAGTGG 947

## RESULT 5

AEE48612

ID AEE48612 standard; DNA; 1227 BP.

AC AEE48612;

DT 23-FEB-2006 (first entry)

DE Shigella dysenteriae shiga-like toxin gene stx-dysenteriae.

XX Microorganism detection; Shiga-like toxin; gene; ds.

OS Shigella dysenteriae.

XX US2005282194-A1.

XX 22-DEC-2005.

XX 29-APR-2005; 2005US-00117858.

XX 17-MAY-2002; 2002US-00150792.

PR (MAYO-) MAYO FOUND MEDICAL EDUCATION &amp; RES.

XX COCKERILL FR, ROSENBLATT JE, SLOAN LM, UHL JR;

XX WPI; 2006-046433/05.

PR Detecting Shiga-like toxin-producing organisms in sample, by detecting fluorescence resonance energy transfer between probes after amplifying and hybridizing toxin nucleic acid in sample with toxin specific primers and labeled probes.

XX Example 2; Fig 1; 25pp; English.

CC The present invention relates to a method (M1) for detecting the presence of absence of Shiga toxin (stx) - or Shiga-like toxin (sltx/sltx2) - producing organisms in sample. The method comprises performing cycling step comprising amplifying and hybridizing steps, using sample, primers and labeled probes for nucleic acid molecule encoding the toxin, and detecting presence of fluorescence resonance energy transfer (FRET) between donor fluorescent moiety of first probe and acceptor fluorescent moiety of second probe. The present sequence is a Shiga-like toxin which was used in a sequence homology alignment to illustrate the invention.

XX Sequence 1227 BP; 334 A; 204 C; 298 G; 389 T; 0 U; 2 Other;

XX Query Match 58.4%; Score 879.6; DB 15; Length 1227;

XX Best Local Similarity 99.7%; Pred. No. 36-253;

XX Matches 879; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 108 GAAGAATTACTTACTTACTTCTGACGCGAAGAGATGATGATGCGTGAATGAT 167  
 DB 66 GAAGAATTACTTACTTACTTCTGACGCGAAGAGATGATGATGCGTGAATGAT 125  
 QY 168 TCGCTCTGCAATAGTACTCATTAACAGACTATTTTCATCAGAGGATGCTTTACTGAT 227  
 DB 126 TCGCTCTGCAATAGTACTCATTAACAGACTATTTTCATCAGAGGATGCTTTACTGAT 185

QY 228 GATTGATAGTGGCAGACAGGGGATATTTGTTGCGAGTTGATGTCAGAGGGATAGATCCAGA 287  
 DB 186 GATTGATAGTGGCAGACAGGGGATATTTGTTGCGAGTTGATGTCAGAGGGATAGATCCAGA 245  
 QY 288 GGAAGGCGGTTTATATATCTACGCGCTTATTTGGAACGAATATTTATATGTCACAG 347  
 DB 246 GGAAGGCGGTTTATATATCTACGCGCTTATTTGGAACGAATATTTATATGTCACAG 305  
 QY 348 ATTGTTAACAGGACAAATATATGTTTATATGCTTGTGATTTTTCACATGTTACTT 407  
 DB 306 ATTGTTAACAGGACAAATATATGTTTATATGCTTGTGATTTTTCACATGTTACTT 365  
 QY 408 TCCAGTACAAACAGCGGTTACATTGTTCTGTGACAGTACATACAGCTTACAGCGTGT 467  
 DB 366 TCCAGTACAAACAGCGGTTACATTGTTCTGTGACAGTACATACAGCTTACAGCGTGT 425  
 QY 468 TGCAGGATCAGTGTACGCGGAGATGCGAGTAAATCCGCAATTCGTTACTTCTTACT 527  
 DB 426 TGCAGGATCAGTGTACGCGGAGATGCGAGTAAATCCGCAATTCGTTACTTCTTACT 485  
 QY 528 GGATTTAATGTCGATATGGAACCTCAGTACGCGAGTCTGTGCAAGAGCGATGTTACG 587  
 DB 486 GGATTTAATGTCGATATGGAACCTCAGTACGCGAGTCTGTGCAAGAGCGATGTTACG 545  
 QY 588 GTTTGTTACTGTGACAGCTGAAAGCTTTACGTTTTCGCAATACAGAGGGATTTCCATC 647  
 DB 546 GTTTGTTACTGTGACAGCTGAAAGCTTTACGTTTTCGCAATACAGAGGGATTTCCATC 605  
 QY 648 AACACTGAGATATCTGAGTGGCGGCTTCTTATGTAATAGCTGTAAGATGTTGATCTTAC 707  
 DB 606 AACACTGAGATATCTGAGTGGCGGCTTCTTATGTAATAGCTGTAAGATGTTGATCTTAC 665  
 QY 708 ATTAAGACTGGGGAAGTTGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 767  
 DB 666 ATTAAGACTGGGGAAGTTGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 725  
 QY 768 TGTAGGAAGAAATTTCTTTGGAAGCAATATATGCAATTTCTGGGAACCGTGGCATTAAT 827  
 DB 726 TGTAGGAAGAAATTTCTTTGGAAGCAATATATGCAATTTCTGGGAACCGTGGCATTAAT 785  
 QY 828 GAATGTCATCATCATGATCGGAGTTCGCGAATGCGATCTGATGAGTTTCCTCAT 887  
 DB 786 GAATGTCATCATCATGATCGGAGTTCGCGAATGCGATCTGATGAGTTTCCTCAT 845  
 QY 888 GTGTCGGGAGATGAGAGAGTCCGTGGGATTACGACATATAATATTTGGGATTCTATC 947  
 DB 846 GTGTCGGGAGATGAGAGAGTCCGTGGGATTACGACATATAATATTTGGGATTCTATC 905  
 QY 948 CACTCTGGGGGCAATTTCTGATGCGGAGAACTATTAGCAGTGG 989  
 DB 906 CACTCTGGGGGCAATTTCTGATGCGGAGAACTATTAGCAGTGG 947

## RESULT 6

ID AAV11404 standard; DNA; 1235 BP.

XX AAV11404;

XX 18-AUG-1998 (first entry)

XX Shiga toxin type 1 PCR fragment p7H1.

XX Histone-tag; toxoid; antibody; treatment; diagnosis; prevention; Stx;

XX haemorrhagic colicitis; haemolytic uremic syndrome; ss.

XX Shigella dysenteriae.

XX WO9811229-A2.

XX 19-MAR-1998.

XX 09-SEP-1997; 97WO-US015836.

XX 10-SEP-1996; 96US-0025637P.  
 PR (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.  
 PA  
 XX Obrien AD, Schmitt CK;  
 PI  
 XX WPI; 1998-207390/18.  
 DR  
 XX  
 XX Purification and isolation of histidine-tagged Shiga toxins - useful in  
 PT vaccines against haemorrhagic colitis and haemolytic uremic syndrome.  
 XX  
 PS Example 1; Fig 6c; 47pp; English.  
 XX  
 XX The Shiga toxin (Stx) PCR fragments (AAV11402-V11406) containing the Stx  
 CC A and B subunits were used to create clones for transformation into  
 CC M15(pREP4) for large scale production of the toxin. Non toxic Shiga  
 CC toxoids, Fusion proteins of His-tagged Shiga toxins/toxoids and  
 CC antibodies can be used in the treatment, diagnosis or prevention of  
 CC infections mediated by toxins of the Stx family. These are associated  
 CC with haemorrhagic colitis and the life-threatening sequelae, haemolytic  
 CC uremic syndrome. Shiga antibodies are also useful for the treatment,  
 CC diagnosis and prevention of disease and infections by pathogenic  
 CC Escherichia coli  
 XX  
 XX Sequence 1235 BP; 346 A; 216 C; 300 G; 373 T; 0 U; 0 Other;  
 SQ  
 Query Match 58.4%; Score 879.6; DB 2; Length 1235;  
 Best Local Similarity 99.5%; Pred. No. 3e-253;  
 Matches 882; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

104 ATCTGAGGAATTATCTAGCTTCTGACTGCTGCACTGCAAGAGCGATGATGATTCGCTGATG 163  
 21 ATCAAGAGGAATTATCTAGCTTCTGACTGCTGCAAGAGCGATGATGATTCGCTGATG 80  
 164 TCATTGGCTGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 223  
 81 TCATTGGCTGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 140  
 224 TGATGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 283  
 141 TGATGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 200  
 284 CAGAGGAAGGCGGCTTAT 343  
 201 CAGAGGAAGGCGGCTTAT 260  
 344 CAGGATTTGTTAAGAGCAAAAT 403  
 261 CAGGATTTGTTAAGAGCAAAAT 320  
 404 CTTTCCAGGTACAAAGCGGTTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 463  
 321 CTTTCCAGGTACAAAGCGGTTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 380  
 464 GTGTGGAGGATGATGCTGATGCGGAGTGCAGATATATGCGCATTCGTTGATCTTCTT 523  
 381 GTGTGGAGGATGATGCTGATGCGGAGTGCAGATATATGCGCATTCGTTGATCTTCTT 440  
 524 ATCTGATTTAATGTCATAGTGAACCTCAGTACGAGCGAGTGTGCGCAAGAGCGATG 583  
 441 ATCTGATTTAATGTCATAGTGAACCTCAGTACGAGCGAGTGTGCGCAAGAGCGATG 500  
 584 TACGTTTGTACTGTGACAGCTGAGCTTTCGTTTTCGCAATATCAGAGGGGATTC 643  
 501 TACGTTTGTACTGTGACAGCTGAGCTTTCGTTTTCGCAATATCAGAGGGGATTC 560  
 644 GTTAAACAGTGAAGATCTCAGTGGGCTTCTTATGTAATGACGCTGGAAGATGTTGATC 703  
 561 GTTAAACAGTGAAGATCTCAGTGGGCTTCTTATGTAATGACGCTGGAAGATGTTGATC 620  
 704 TTACATTGAACCTGGGAGGTTGATGAGCGTCTGCGCTGATCATGAGCAAGACTCTG 763

DB 621 TTACATTGAACCTGGGAGGTTGATGAGCGTCTGCTGACTATCATGACAAAGCTCTG 680  
 QY 764 TTGCTGTAGAGAAATTTCTTTTGGAGCATTAATGCAATTTCTGGAGCGGTGATTA 823  
 DB 681 TTGCTGTAGAGAAATTTCTTTTGGAGCATTAATGCAATTTCTGGAGCGGTGATTA 740  
 QY 824 TACTGAATTTGTCATCATGATGATGCGAGTTTCCAGATGCAATCTGATGATTTCTT 883  
 DB 741 TACTGAATTTGTCATCATGATGATGCGAGTTTCCAGATGCAATCTGATGATTTCTT 800  
 QY 884 CTATGTCGCGGAGATGGAAGAGTCCGTTGGAATTAGCCAAATTAATATTTGTTGGATT 943  
 DB 801 CTATGTCGCGGAGATGGAAGAGTCCGTTGGAATTAGCCAAATTAATATTTGTTGGATT 860  
 QY 944 CATCCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTGG 989  
 DB 861 CATCCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTGG 906

RESULT 7  
 AAT42671  
 ID AAT42671 standard; DNA; 2126 BP.  
 AC AAT42671;  
 AC  
 AC 26-FEB-1997 (first entry)  
 DT  
 XX  
 XX Maltose binding protein/VT1 A subunit fusion construct.  
 DE  
 XX Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine;  
 KM haemolytic uremic syndrome; detection; ss.  
 XX  
 XX Escherichia coli.  
 OS  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2125 /\*tag=a  
 FT /product= "MBP/VT1 fusion protein"  
 FT  
 XX  
 PN W09630043-A1.  
 PD 03-OCT-1996.  
 PD  
 XX  
 XX 25-MAR-1996; 96WO-US004093.  
 PF  
 XX 24-MAR-1995; 95US-00410058.  
 PR  
 XX (OPHI-) OPHIDIUM PHARM INC.  
 PA  
 PI Carroll SB, Stafford DC, Padhye NV;  
 PI  
 XX WPI; 1996-505779/50.  
 DR P-PSDB; AAM06411.  
 DR  
 XX  
 PT Compn. contg. neutralising antitoxin against E.coli vero-toxin - used to  
 PT treat intoxicated individuals, and as a prophylactic against diarrhoeal  
 PT disease or extra-intestinal complications of E.coli infection.  
 XX  
 XX Example 6; Page 67-70; 101pp; English.  
 PS  
 XX Compositions containing neutralising antitoxin against one or more E.  
 CC coli verotoxin (VT) can be used to treat intoxicated adults and children  
 CC with enteric bacterial infections. They may also be used as prophylactics  
 CC e.g. as a vaccine, against diarrhoeal disease or the development of extra  
 CC -intestinal complications of E.coli infection, especially haemolytic  
 CC uremic syndrome. The antitoxin can also be used to detect E. coli VT in  
 CC a sample. The VT is recombinant, preferably a fusion protein containing a  
 CC non-VT protein sequence and part of the E.coli VT1 or VT2 sequence. This  
 CC sequence encodes a maltose binding protein/VT1 A subunit fusion protein  
 XX  
 XX Sequence 2126 BP; 591 A; 463 C; 546 G; 526 T; 0 U; 0 Other;  
 SQ  
 Query Match 58.4%; Score 879.4; DB 2; Length 2126;



```

Db      1298 ATGTCAATTCGCTCTGCAATAGTACTCCATTAGACGATATTCATGAGAGGATACGCTT 1357
QY      221 TACTGATGATTTGATAGTGGACAGAGGGGATTAATTTGTTGAGTTGATGTCAGAGGGATAG 280
Db      1358 TACTGATGATTTGATAGTGGCTCAGAGGGATTAATTTGTTGAGTTGATGTCAGAGGGATAG 1417
QY      281 ATCCAGAGGAGGCGGCTTTAATATCTACGGCTTAATTTGTTGAGCGAATTAATTTATATG 340
Db      1418 ATCCAGAGGAGGCGGCTTTAATATCTACGGCTTAATTTGTTGAGCGAATTAATTTATATG 1477
QY      341 TGACAGATTTGTTAACAAGACAAATATATGTTTTTATATGCTTTCGCTGATTTTTCATG 400
Db      1478 TGACAGATTTGTTAACAAGACAAATATATGTTTTTATATGCTTTCGCTGATTTTTCATG 1537
QY      401 TTACCTTTCCAGGTACACAGCGGTTTACATTTGCTGCTGACAGTATATACCAAGCTTAC 460
Db      1538 TTACCTTTCCAGGTACACAGCGGTTTACATTTGCTGCTGACAGTATATACCAAGCTTAC 1597
QY      461 AGCGTGTGAGGAGATCAGTCTGACGGGGATGACAGATTAATTCGCATTCGTTGACTTACT 520
Db      1598 AGCGTGTGAGGAGATCAGTCTGACGGGGATGACAGATTAATTCGCATTCGTTGACTTACT 1657
QY      521 CTATCTCGATTTTAATGTCGATATGTCGATACCTCACTGACGAGCTCTGTGGCAAGAGCGA 580
Db      1658 CTATCTCGATTTTAATGTCGATATGTCGATACCTCACTGACGAGCTCTGTGGCAAGAGCGA 1717
QY      581 TGTACGCTTTGTTTACTGTGACAGCTGACCTTACCTTTCCGCAATATACAGAGGGAT 640
Db      1718 TGTACGCTTTGTTTACTGTGACAGCTGACCTTACCTTTCCGCAATATACAGAGGGAT 1777
QY      641 TTGCTACACACAGTGAATGTCGATGTCGAGGCTTCTTAATGATACGCTGGAAGATGTTG 700
Db      1778 TTGCTACACACAGTGAATGTCGATGTCGAGGCTTCTTAATGATACGCTGGAAGATGTTG 1837
QY      701 ATCTTAATTTGAATGTCGAGGAGGTCGATGTCGAGGCTTCTTAATGATACGCTGGAAGAT 760
Db      1838 ATCTTAATTTGAATGTCGAGGAGGTCGATGTCGAGGCTTCTTAATGATACGCTGGAAGAT 1897
QY      761 CTGTTCTGTGAGGAATTTCTTTTGGAGCATTAATGCAATTTCTGGAGAGCGTGGCAT 820
Db      1898 CTGTTCTGTGAGGAATTTCTTTTGGAGCATTAATGCAATTTCTGGAGAGCGTGGCAT 1957
QY      821 TAATACGATTTGTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 880
Db      1958 TAATACGATTTGTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 2017
QY      881 CTCTATGTCGTCGAGATGAGAGATCCGTCGATTTACGACAAATTAATTTGTCGG 940
Db      2018 CTCTATGTCGTCGAGATGAGAGATCCGTCGATTTACGACAAATTAATTTGTCGG 2077
QY      941 ATTCATCCACTCTGCGGGCAATTTCTGATGCGCAGAACTATTAGCAGTGG 989
Db      2078 ATTCATCCACTCTGCGGGCAATTTCTGATGCGCAGAACTATTAGCAGTGG 2126

RESULT 9
ABK11797
ID      ABK11797 standard; DNA; 2127 BP.
XX
XX      ABK11797:
AC
XX      05-JUN-2002 (first entry)
DT
XX      cDNA encoding MBPNVT1-A fusion protein.
XX
XX      Verotoxin; MBPNVT1-A; antitoxin; antidiarrheal; antibacterial;
KM      haemolytic; vaccine; haemorrhagic cystitis; balantitis;
KM      haemolytic uremic syndrome; thrombotic thrombocytopenic purpura; ss.
XX      Escherichia coli.
XX
XX      Key      Location/Qualifiers
FH      CDS      1..2127
FT

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FT      /*tag= A
FT      /product= "MBPNVT1-A fusion protein"
XX
XX      US2002012658-A1.
XX      31-JAN-2002.
XX
XX      16-JUN-1999; 99US-00334477.
XX
XX      13-MAR-1997; 97US-00816977.
XX
XX      (WILLIAMS J A.
XX      (BYRNE J M.
XX      (PUGH C S G.
XX
XX      Williams JA, Byrne JM, Pugh CSG;
XX
XX      WPI, 2002-205094/26.
XX      P-PSDB; AAU77826.
XX
XX      New recombinant expression vector encoding affinity tag and Escherichia
XX      coli type 1 or type 2 verotoxin, useful for treating or preventing
XX      diseases due to E. coli verotoxins and in producing vaccines.
XX
XX      Example 6; Page 54-57; 98pp; English.
XX
XX      This invention relates to a recombinant expression vector encoding an
XX      affinity tag and protein comprising at least a portion of a bacterial
XX      toxin consisting of Escherichia coli type 1 or type 2 verotoxin. The
XX      expression vector can be used to produce recombinant verotoxin protein
XX      which can be used to create a vaccine against diseases caused by E. coli
XX      such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins
XX      are useful for treating humans and animals intoxicated with a bacterial
XX      toxin, particularly E. coli verotoxin. The antitoxins may also be used in
XX      the preventative treatment and in diagnostic assays to detect the
XX      presence of a toxin in a sample. The polypeptides derived from E. coli
XX      verotoxins are useful as immunogens for the production of vaccines,
XX      including multivalent vaccines and antitoxins, which can be administered
XX      to a subject at risk of diarrhoeal disease or at risk of developing extra
XX      -intestinal complications of E. coli infections, e.g. haemolytic uremic
XX      syndrome, thrombotic thrombocytopenic purpura. The present sequence
XX      represents the cDNA encoding the MBPNVT1-A protein of the invention. This
XX      fusion protein was created to facilitate purification of the recombinant
XX      proteins of the invention
XX
XX      Sequence 2127 BP; 592 A; 463 C; 546 G; 526 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      58.4%; Score 879.4; DB 6; Length 2127;
XX      Best Local Similarity 99.3%; Pred. No. 4,7e-253;
XX      Matches 883; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
QY      101 CAGATCTGAAGAATTTTACCTTGAAGCTTCTGACCTGCAAGACGATATGATTCGCTGA 160
Db      1238 CAGAAATTCAGGAATTTTACCTTGAAGCTTCTGACCTGCAAGACGATATGATTCGCTGA 1297
QY      161 ATGTCAATTCGCTCTGCAATATGTCATCCATTACAGACTTTTATATAGAGGATACGCTT 220
Db      1298 ATGTCAATTCGCTCTGCAATATGTCATCCATTACAGACTTTTATATAGAGGATACGCTT 1357
QY      221 TACTGATGATTTGATAGTGGACAGAGGGATTAATTTGTTGAGTTGATGTCAGAGGGATAG 280
Db      1358 TACTGATGATTTGATAGTGGCTCAGAGGGATTAATTTGTTGAGTTGATGTCAGAGGGATAG 1417
QY      281 ATCCAGAGGAGGCGGCTTTAATATCTACGGCTTAATTTGTTGAGCGAATTAATTTATATG 340
Db      1418 ATCCAGAGGAGGCGGCTTTAATATCTACGGCTTAATTTGTTGAGCGAATTAATTTATATG 1477
QY      341 TGACAGATTTGTTAACAAGACAAATATATGTTTTTATATGCTTTCGCTGATTTTTCATG 400
Db      1478 TGACAGATTTGTTAACAAGACAAATATATGTTTTTATATGCTTTCGCTGATTTTTCATG 1537
QY      401 TTACCTTTCCAGGTACACAGCGGTTTACATTTGCTGCTGACAGTATATACCAAGCTTAC 460

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Db 1538 TTACCTTTCAAGGTACAAAGCGGTTACATGTCGTGACAGTAGTATACCAAGTTAC 1597  
 QY 461 AGCGGTGGCAGGGATCATGTCGTACGGGATGAGATTAATCGCATTCGTGTGACTCTT 520  
 Db 1598 AGCGGTGGCAGGGATCATGTCGTACGGGATGAGATTAATCGCATTCGTGTGACTCTT 1657  
 QY 521 CTTATCTGGATTTATATGTCGATATGAGAACCTCACTAGCCAGTCTGTGCAAGAGCA 580  
 Db 1658 CTTATCTGGATTTATATGTCGATATGAGAACCTCACTAGCCAGTCTGTGCAAGAGCA 1717  
 QY 581 TGTACGGTTTGTACTGTGACAGCTGAAGCTTTACGTTTTCGGCAATACAGAGGGAT 640  
 Db 1718 TGTACGGTTTGTACTGTGACAGCTGAAGCTTTACGTTTTCGGCAATACAGAGGGAT 1777  
 QY 641 TTCCGACAACTGATGATCTCACTGCGGCTTATATGATGATGCTGCAAGATGTTG 700  
 Db 1778 TTCCGACAACTGATGATCTCACTGCGGCTTATATGATGATGCTGCAAGATGTTG 1837  
 QY 701 ATCTTACATTTGAATCGGGAAGTTGAGTAGCGTCTGCTGACTATCATGAGACAAACT 760  
 Db 1838 ATCTTACATTTGAATCGGGAAGTTGAGTAGCGTCTGCTGACTATCATGAGACAAACT 1897  
 QY 761 CTGTTGCTGAGGAAGAAATTTCTTTGGAAGCATTATGCAATTTCTGGGAACCGTGCAT 820  
 Db 1898 CTGTTGCTGAGGAAGAAATTTCTTTGGAAGCATTATGCAATTTCTGGGAACCGTGCAT 1957  
 QY 821 TAAATCTGAATTTGTCATCATCATGATGCGGAGTTCGCGAATGTCATCTGATGAGTTTC 880  
 Db 1958 TAAATCTGAATTTGTCATCATCATGATGCGGAGTTCGCGAATGTCATCTGATGAGTTTC 2017  
 QY 881 CTTTATGATGTCGCGAGATGGAAGATCCGTGGGATTACGCAATTAATAATTTGTTGGG 940  
 Db 2018 CTTTATGATGTCGCGAGATGGAAGATCCGTGGGATTACGCAATTAATAATTTGTTGGG 2077  
 QY 941 ATTCAATCACTTTGGGGCAATTTCTGATGCGGAGATTTAGCAATTTAGCACTG 989  
 Db 2078 ATTCAATCACTTTGGGGCAATTTCTGATGCGGAGATTTAGCAATTTAGCACTG 2126  
 RESULT 10  
 ADL25577  
 ID ADL25577 standard. DNA; 1227 BP.  
 XX  
 AC ADL25577;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE S. sonnei shiga toxin gene stx-sonnei.  
 XX  
 KM Shiga toxin; ds; gene; fluorescence resonance energy transfer; FRET;  
 KM gastrointestinal disease; dysentery.  
 XX  
 OS Shigella sonnei.  
 XX  
 PN US2003215814-A1.  
 XX  
 PD 20-NOV-2003.  
 XX  
 PF 17-MAY-2002; 2002US-00150792.  
 XX  
 PR 17-MAY-2002; 2002US-00150792.  
 XX  
 PA (COCK/) COCKERILL F R.  
 PA (ROSE/) ROSENBLATT J E.  
 PA (SLOA/) SLOAN L.  
 PA (UHLJ/) UHL J R.  
 PI Cockerill FR, Rosenblatt JE, Sloan L, Uhl JR;  
 DR WPI; 2003-902026/82.  
 XX  
 PT Detecting presence or absence of Shiga toxin producing organisms in  
 PT biological sample, by amplifying nucleic acid encoding Shiga toxin with

PT pair of stx1 primers and detecting fluorescence resonance energy  
 PT transfer.  
 XX  
 PS Example 2; Fig 1; 24pp: English.  
 CC The invention relates to detecting the presence or absence of Shiga toxin  
 CC or Shiga-like toxin producing organisms in a biological sample involving  
 CC amplifying nucleic acid encoding Shiga toxin with a pair of stx1 primers,  
 CC detecting the amplified product with labelled stx1 probes, and detecting  
 CC the presence or absence of fluorescence resonance energy transfer (FRET).  
 CC Also included is an article of manufacture comprising the stx1 primers  
 CC and probes and a donor fluorescent moiety and corresponding fluorescent  
 CC moiety or a pair of stx2 primers, a pair of stx2 probes and a donor  
 CC fluorescent moiety and corresponding fluorescent moiety. The method is  
 CC useful for detecting the presence or absence of one or more Shiga toxin  
 CC or Shiga-like toxin producing organisms e.g. Escherichia coli (especially  
 CC gastrointestinal disease causing strains) and Shigella (causative agent  
 CC of dysentery) in a biological sample which is a stool sample or body  
 CC fluids from an individual. The method is rapid and specific in detecting  
 CC the Shiga toxin from biological samples. The present sequence is a  
 CC bacterial shiga toxin or shiga-like toxin gene used to design the primers  
 CC and probes of the invention.  
 XX  
 SQ Sequence 1227 BP; 335 A; 203 C; 297 G; 392 T; 0 U; 0 Other;  
 Query Match 58.3%; Score 879; DB 11; Length 1227;  
 Best Local Similarity 99.4%; Pred. No. 4.6e-253;  
 Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 103 GATCTGAAGAAATTTACCTTATGATCTCTGACATGCAAGAGCTATGATGCTGAT 162  
 Db 61 GTTCGAGGAAGAAATTTACCTTATGATCTCTGACATGCAAGAGCTATGATGCTGAT 120  
 QY 163 GTCAATGCTCTGCAATAGTACTCATACAGACTATTTTATCATGAGAGTACGTCCTTA 222  
 Db 121 GTCAATGCTCTGCAATAGTACTCATACAGACTATTTTATCATGAGAGTACGTCCTTA 180  
 QY 223 CTGATGATTTGATGTCGACAGGGGATTAATTTGTTGCACTGATGTCAGAGGGATAGT 282  
 Db 181 CTGATGATTTGATGTCGACAGGGGATTAATTTGTTGCACTGATGTCAGAGGGATAGT 240  
 QY 283 CCAGAGGAAGGGGGTTTAAATCTACGGCTTATGTTGTAAGCAATTAATTTATATG 342  
 Db 241 CCAGAGGAAGGGGGTTTAAATCTACGGCTTATGTTGTAAGCAATTAATTTATATG 300  
 QY 343 ACAGGATTTGTTAAGAGACAAATTAATGTTTATATGCTTGTGCTGATTTTACATGTT 402  
 Db 301 ACAGGATTTGTTAAGAGACAAATTAATGTTTATATGCTTGTGCTGATTTTACATGTT 360  
 QY 403 ACCTTTCCAGGTACACAGCGGTTACATTTGTCGTGACAGTACTATACACGTTACAG 462  
 Db 361 ACCTTTCCAGGTACACAGCGGTTACATTTGTCGTGACAGTACTATACACGTTACAG 420  
 QY 463 CGTGTGAGGAGATCAGTCGACAGGGGATGAGATTAATGCGCATTCGTTGACTACTTCT 522  
 Db 421 CGTGTGAGGAGATCAGTCGACAGGGGATGAGATTAATGCGCATTCGTTGACTACTTCT 480  
 QY 523 TATCTGATTTAATGTCGCATAGTGAACCTCACTGACGAGCTGTGGCAAGCGATG 582  
 Db 481 TATCTGATTTAATGTCGCATAGTGAACCTCACTGACGAGCTGTGGCAAGCGATG 540  
 QY 583 TTACGGTTTGTACTGTGACAGCTGAGCTTTAGCTTTTCCGCAATACAGAGGGGATTT 642  
 Db 541 TTACGGTTTGTACTGTGACAGCTGAGCTTTAGCTTTTCCGCAATACAGAGGGGATTT 600  
 QY 643 CGTACACACTGATGATCTCAGTGGGGGCTTTATGTAATGATGCTGGAAGATGTTGAT 702  
 Db 601 CGTACACACTGATGATCTCAGTGGGGGCTTTATGTAATGATGCTGGAAGATGTTGAT 660  
 QY 703 CTTACATTTGAATCGGGAAGGTTGATAGCGTCTGCTGACTATCATGACAAAGACTCT 762  
 Db 661 CTTACATTTGAATCGGGAAGGTTGATAGCGTCTGCTGACTATCATGACAAAGACTCT 720



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QY 763 GTTCGTGTAGAGAAATTTCTTTGGAGCAATTAATCTTGGGAGCGTGCAATTA 822
DB 721 GTTCGTGTAGAGAAATTTCTTTGGAGCAATTAATCTTGGGAGCGTGCAATTA 780
QY 823 ATATCTGAATTTGATCATCATGATCCGAGTTGCCAGATGCGATCTGATGATTTCT 882
DB 781 ATATCTGAATTTGATCATCATGATCCGAGTTGCCAGATGCGATCTGATGATTTCT 840
QY 883 TCTATGTGTCGGGAGATGAGATCCGTGGGATTAACGACATTAATATTGGGAT 942
DB 841 TCTATGTGTCGGGAGATGAGATCCGTGGGATTAACGACATTAATATTGGGAT 900
QY 943 TCATCCACTCTGGGGCAATTTCTGATGCGAGAACTATTAGCACTG 989
DB 901 TCATCCACTCTGGGGCAATTTCTGATGCGAGAACTATTAGCACTG 947

RESULT 11
ID AEE48613 standard; DNA; 1227 BP.
XX AEE48613;
AC AEE48613;
XX
XX 23-FEB-2006 (first entry)
XX
XX Shigella sonnei shiga-like toxin gene stx-sonnei.
XX
XX Microorganism detection; Shiga-like toxin; gene; ds.
XX
XX Shigella sonnei.
XX
XX US2005282194-A1.
XX
XX 22-DEC-2005.
XX
XX 29-APR-2005; 2005US-00117858.
XX
XX 17-MAY-2002; 2002US-00150792.
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
XX Cockerill FR, Rosenblatt JE, Sloan LM, Uhl JR;
XX
XX WPI; 2006-046433/05.
XX
XX
XX Detecting Shiga-like toxin-producing organisms in sample, by detecting
XX fluorescence resonance energy transfer between probes after amplifying
XX PT and hybridizing toxin nucleic acid in sample with toxin specific primers
XX PT and labeled probes.
XX
XX Example 2; Fig 1; 25pp; English.
XX
XX The present invention relates to a method (M1) for detecting the presence
XX CC or absence of Shiga toxin (stx) - or Shiga-like toxin (stx1/stx2) -
XX CC producing organisms in sample. The method comprises performing cycling
XX CC step comprising amplifying and hybridizing steps, using sample, primers
XX CC and labeled probes for nucleic acid molecule encoding the toxin, and
XX CC detecting presence of fluorescence resonance energy transfer (FRET)
XX CC between donor fluorescent moiety of first probe and acceptor fluorescent
XX CC moiety of second probe. The present sequence is a Shiga-like toxin which
XX CC was used in a sequence homology alignment to illustrate the invention.
XX
XX Sequence 1227 BP; 335 A; 203 C; 297 G; 392 T; 0 U; 0 Other;
SQ

Query Match 58.3%; Score 879; DB 15; Length 1227;
Best Local Similarity 99.4%; Pred. No. 4.6e-253;
Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 103 GATCTGAAGAAATTTACTTGAAGCTTCTGCACTGCAAGAGCTATGTAGATTGCTGAAT 162
DB 61 GTTCGGAAGAAATTTACTTGAAGCTTCTGCACTGCAAGAGCTATGTAGATTGCTGAAT 120
QY 163 GTCATTCGCTCTGCAATAGACTTCATTCACACTTATTTTCATCAGAGAGTACGCTTTTA 222
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DB 121 GTTCATTCCTCTGCAATAGACTTCATTCACACTTATTTTCATCAGAGAGTACGCTTTTA 180
QY 223 CTGATGATTTGATAGTGGCAAGGGGATTAATTTGTTTGAGTTGATGTCAGAGGGATAGAT 282
DB 181 CTGATGATTTGATAGTGGCAAGGGGATTAATTTGTTTGAGTTGATGTCAGAGGGATAGAT 240
QY 283 CCAGAGAGAGGGCGGTTTAATTAATCTACGCGCTTATTTGTAACGAATTAATTTATATGTC 342
DB 241 CCAGAGAGAGGGCGGTTTAATTAATCTACGCGCTTATTTGTAACGAATTAATTTATATGTC 300
QY 343 AAGAGATTTGTTTAACAGAGCAAAATATGTTTTTATTCCTTTCGATTTTTCACATGTT 402
DB 301 AAGAGATTTGTTTAACAGAGCAAAATATGTTTTTATTCCTTTCGATTTTTCACATGTT 360
QY 403 ACCTTTCCAGTACAGAGCGGTTTCAATTTGTCGTGTCAGTAGCTATTAACAGTTTACG 462
DB 361 ACCTTTCCAGTACAGAGCGGTTTCAATTTGTCGTGTCAGTAGCTATTAACAGTTTACG 420
QY 463 CGTGTTCAGAGGATCAGTGTGTCAGGGGATGTCAGATTAATTCGCATTCCTTTCCT 522
DB 421 CGTGTTCAGAGGATCAGTGTGTCAGGGGATGTCAGATTAATTCGCATTCCTTTCCT 480
QY 523 TATCTGATTTTAATGTCGATAGTGAACCTCAGTACGAGGCTGTGGCAAGAGCATG 582
DB 481 TATCTGATTTTAATGTCGATAGTGAACCTCAGTACGAGGCTGTGGCAAGAGCATG 540
QY 583 TTACGGTTTGTACTGTCGACAGCTGAAGCTTTTACGTTTTCGCAATACAGAGGGGATTT 642
DB 541 TTACGGTTTGTACTGTCGACAGCTGAAGCTTTTACGTTTTCGCAATACAGAGGGGATTT 600
QY 643 CGTACAACTGAGATGATCTCAGTGGCGGCTTTTATGATTAATCAGTCTGAAGATGTTAT 702
DB 601 CGTACAACTGAGATGATCTCAGTGGCGGCTTTTATGATTAATCAGTCTGAAGATGTTAT 660
QY 703 CTTACATTTGAACTGGGGGAGGTTGAGTAGCTCCGCGCTGACATTCATGAGCAAGACTCT 762
DB 661 CTTACATTTGAACTGGGGGAGGTTGAGTAGCTCCGCGCTGACATTCATGAGCAAGACTCT 720
QY 763 GTTCGTGTAGAGAAATTTCTTTGGAGCAATTAATCTTGGGAGCGTGCAATTA 822
DB 721 GTTCGTGTAGAGAAATTTCTTTGGAGCAATTAATCTTGGGAGCGTGCAATTA 780
QY 823 ATATCTGAATTTGATCATCATGATCCGAGTTGCCAGATGCGATCTGATGATTTCT 882
DB 781 ATATCTGAATTTGATCATCATGATCCGAGTTGCCAGATGCGATCTGATGATTTCT 840
QY 883 TCTATGTGTCGGGAGATGAGATCCGTGGGATTAACGACATTAATATTGGGAT 942
DB 841 TCTATGTGTCGGGAGATGAGATCCGTGGGATTAACGACATTAATATTGGGAT 900
QY 943 TCATCCACTCTGGGGCAATTTCTGATGCGAGAACTATTAGCACTG 989
DB 901 TCATCCACTCTGGGGCAATTTCTGATGCGAGAACTATTAGCACTG 947

RESULT 12
ADL25575
ID ADL25575 standard; DNA; 1227 BP.
XX ADL25575;
AC ADL25575;
XX
XX 20-MAY-2004 (first entry)
XX
XX Bacteriophage h30 shiga toxin gene stx1.
XX
XX Shiga toxin; ds; gene; fluorescence resonance energy transfer; FRET;
XX km gastrointestinal disease; dysentery.
XX
XX Bacteriophage h30.
XX
XX US2003215814-A1.
XX
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PD 20-NOV-2003.  
 XX  
 PF 17-MAY-2002; 2002US-00150792.  
 XX  
 PR 17-MAY-2002; 2002US-00150792.  
 XX  
 PA (COCK/) COCKERILL F R.  
 PA (ROSE/) ROSENBLATT J E.  
 PA (SLOA/) SLOAN L.  
 PA (UHLJ/) UHL J R.  
 XX  
 PI Cockerill FR, Rosenblatt JE, Sloan L, Uhl JR;  
 XX  
 DR WPI; 2003-902026/82.  
 XX  
 PT Detecting presence or absence of Shiga toxin producing organisms in  
 PT biological sample, by amplifying nucleic acid encoding Shiga toxin with  
 PT pair of stx1 primers and detecting fluorescent resonance energy  
 PT transfer.  
 XX  
 PS Example 2; Fig 1; 24pp; English.  
 XX  
 CC The invention relates to detecting the presence or absence of Shiga toxin  
 CC or Shiga-like toxin producing organisms in a biological sample involving  
 CC amplifying nucleic acid encoding Shiga toxin with a pair of stx1 primers,  
 CC detecting the amplified product with labelled stx1 probes, and detecting  
 CC the presence or absence of fluorescence resonance energy transfer (FRET).  
 CC Also included is an article of manufacture comprising the stx1 primers  
 CC and probes and a donor fluorescent moiety and corresponding fluorescent  
 CC moiety or a pair of stx2 primers, a pair of stx2 probes and a donor  
 CC fluorescent moiety and corresponding fluorescent moiety. The method is  
 CC useful for detecting the presence or absence of one or more Shiga toxin  
 CC or Shiga-like toxin producing organism e.g. Escherichia coli (especially  
 CC gastrointestinal disease causing strains) and Shigella (causative agent  
 CC of dysentery) in a biological sample which is a stool sample or body  
 CC fluids from an individual. The method is rapid and specific in detecting  
 CC the Shiga toxin from biological samples. The present sequence is a  
 CC bacterial shiga toxin or shiga-like toxin gene used to design the primers  
 CC and probes of the invention.  
 XX  
 SQ Sequence 1227 BP; 334 A; 205 C; 298 G; 390 T; 0 U; 0 Other;  
 XX  
 Query Match 58.3%; Score 878.8; DB 11; Length 1227;  
 Best Local Similarity 99.8%; Pred. No. 5.2e-253;  
 Matches 880; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 108 GAAGGAATTTACCTAGACTCTCGACGCAAGACGATGATGCTGCTGATGCTAT 167  
 DB 66 GAAGGAATTTACCTAGACTCTCGACGCAAGACGATGATGCTGCTGATGCTAT 125  
 QY 168 TCGCTCTGCAATAGTAGTCTCCATTACAGACTATTTTCATCAGAGAGTACGCTTTACTGAT 227  
 DB 126 TCGCTCTGCAATAGTAGTCTCCATTACAGACTATTTTCATCAGAGAGTACGCTTTACTGAT 185  
 QY 228 GATTGATAGTGGCAAGGGGATATTTGTTGCACTGATGTCAGAGGATGATCCAGA 287  
 DB 186 GATTGATAGTGGCTCAGAGGATATTTGTTGCACTGATGTCAGAGGATGATCCAGA 245  
 QY 288 GGAAGGGGGGTTTATATATATACGCGCTATTTGTAAGCAATATATTTATATGAGACAG 347  
 DB 246 GGAAGGGGGGTTTATATATATACGCGCTATTTGTAAGCAATATATTTATATGAGACAG 305  
 QY 348 ATTGTTTACAGAGCAAAATATGTTTTTATCGCTTTGCTGATTTTTCACATGTTACCTT 407  
 DB 306 ATTGTTTACAGAGCAAAATATGTTTTTATCGCTTTGCTGATTTTTCACATGTTACCTT 365  
 QY 408 TTCAGGTACACAGAGGCTTACATTTCTGCGACAGTATGCTATACACAGTTACAGCGCT 467  
 DB 366 TTCAGGTACACAGAGGCTTACATTTCTGCGACAGTATGCTATACACAGTTACAGCGCT 425  
 QY 468 TGCAGAGTACAGTCTGACGGGATGACAGATTAATGACCATTCGTTGACCTACTTCTTACT 527  
 DB 426 TGCAGAGTACAGTCTGACGGGATGACAGATTAATGACCATTCGTTGACCTACTTCTTACT 485

QY 528 GGATTTATGTCGCATAGTAGTGAACCTTCACAGCAGTCTGTGGCAAGACGATGTTACG 587  
 DB 486 GGATTTATGTCGCATAGTAGTGAACCTTCACAGCAGTCTGTGGCAAGACGATGTTACG 545  
 QY 588 GTTGTACTGTGACACGCTGACGCTTACGTTTTCGCAATATACAGGGGATTTGCTAC 647  
 DB 546 GTTGTACTGTGACACGCTGACGCTTACGTTTTCGCAATATACAGGGGATTTGCTAC 605  
 QY 648 AACACTGATGATCTGACGCGGGGCTTATGTAATGACTGCAAGATGTTGATCTTAC 707  
 DB 606 AACACTGATGATCTGACGCGGGGCTTATGTAATGACTGCAAGATGTTGATCTTAC 665  
 QY 708 ATTGAACGCGGGAAGGTTGAGTACGCTGCTGCTGCACTATACAGCAAGCTGTGTCG 767  
 DB 666 ATTGAACGCGGGAAGGTTGAGTACGCTGCTGCTGCACTATACAGCAAGCTGTGTCG 725  
 QY 768 TGTAGCAAGATTTCTTTTGGAAAGCATTAATGCAATTTCTGGAAAGCTGGCATTAATCT 827  
 DB 726 TGTAGCAAGATTTCTTTTGGAAAGCATTAATGCAATTTCTGGAAAGCTGGCATTAATCT 785  
 QY 828 GAATTCATCATCATCATCATCGAGTTCGAGATGAGATGATGATGATGATGATGATGAT 887  
 DB 786 GAATTCATCATCATCATCATCGAGTTCGAGATGAGATGAGATGATGATGATGATGATGAT 845  
 QY 888 GTGTCCGCGAGATGGAAGAGTCCGTGGATTAACGACAAATTAATTTGTGGATTCATC 947  
 DB 846 GTGTCCGCGAGATGGAAGAGTCCGTGGATTAACGACAAATTAATTTGTGGATTCATC 905  
 QY 948 CACTCTGGGGCAATTTGATGCGGCAACTATTAAGCAGTGG 989  
 DB 906 CACTCTGGGGCAATTTGATGCGGCAACTATTAAGCAGTGG 947  
 RESULT 13  
 AEB48611  
 ID AEB48611 standard; DNA; 1227 BP.  
 XX  
 AC AEB48611;  
 XX  
 DT 23-FEB-2006 (first entry)  
 XX  
 DE Bacteriophage h30 shiga-like toxin gene stx1.  
 XX  
 KW Microorganism detection; Shiga-like toxin; gene; ds.  
 XX  
 OS Bacteriophage h30.  
 XX  
 FN US2005282194-A1.  
 XX  
 PD 22-DEC-2005.  
 XX  
 PF 29-APR-2005; 2005US-00117858.  
 XX  
 PR 17-MAY-2002; 2002US-00150792.  
 XX  
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
 PA Cockerill FR, Rosenblatt JE, Sloan LM, Uhl JR;  
 PI WPI; 2006-046433/05.  
 DR  
 XX  
 XX  
 PT Detecting Shiga-like toxin-producing organisms in sample, by detecting  
 PT fluorescence resonance energy transfer between probes after amplifying  
 PT and hybridizing toxin nucleic acid in sample with toxin specific primers  
 PT and labeled probes.  
 XX  
 PS Example 2; Fig 1; 25pp; English.  
 XX  
 CC The present invention relates to a method (M1) for detecting the presence  
 CC or absence of Shiga toxin (stx)- or Shiga-like toxin (stx1/stx2) -  
 CC producing organisms in sample. The method comprises performing cycling  
 CC step comprising amplifying and hybridizing steps, using sample, primers

CC and labeled probes for nucleic acid molecule encoding the toxin, and  
CC detecting presence of fluorescence resonance energy transfer (FRET)  
CC between donor fluorescent moiety of first probe and acceptor fluorescent  
CC moiety of second probe. The present sequence is a Shiga-like toxin which  
CC was used in a sequence homology alignment to illustrate the invention.

Query Match	Score	DB	Length
58.3%	878.8	15	1227

Matches	880;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
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Qy	108	GAAGAAATTACCTTAAGACTTCTGCACCTGCAAGACGATATGAATTGCGCGAAATGCAT	167
Db	66	GAAGAAATTACCTTAAGACTTCTGCACCTGCAAGACGATATGAATTGCGCGAAATGCAT	125
Qy	168	TGCGCTCTGCAATAGTAGTACTCCATTACAGACTATTTTCATCAGAGGTACGCTTTACTGAT	227
Db	126	TGCGCTCTGCAATAGGTACTCCATTACAGACTATTTTCATCAGAGGTACGCTTTACTGAT	185
Qy	228	GATGTATATGTGCTCAGCGGATTAATTTGTTGCGAGTTGATGTCAGAGGATTAAGTCCAGA	287
Db	186	GATGTATATGTGCTCAGCGGATTAATTTGTTGCGAGTTGATGTCAGAGGATTAAGTCCAGA	245
Qy	288	GGAAAGGCGGTTTAATTAATCTACGGCTTAATGTTTGAAGAAATAATTATATGTGACAGG	347
Db	246	GGAAAGGCGGTTTAATTAATCTACGGCTTAATGTTTGAAGAAATAATTATATGTGACAGG	305
Qy	348	ATTGTTTAAACAGACCAATATGTTTTTTATGCTGCTTGCTGATTTTTCACATGTTACCTT	407
Db	306	ATTGTTTAAACAGACCAATATGTTTTTTATGCTGCTTGCTGATTTTTCACATGTTACCTT	365
Qy	408	TCCAGGTACAAACAGCGGTTACATTGTCGTGGACGTGCTATPACACAGTTACAGCGGT	467
Db	366	TCCAGGTACAAACAGCGGTTACATTGTCGTGGACGTGCTATPACACAGTTACAGCGGT	425
Qy	468	TGCAGGATCAGTCTGACGGGGATGCAATTAATGCAATTCGTTGACTACTTCTTATCT	527
Db	426	TGCAGGATCAGTCTGACGGGGATGCAATTAATGCAATTCGTTGACTACTTCTTATCT	485
Qy	528	GGATTTAATGTGGCAATGTGGAACCTCCTACGTACGAGCTGTGGCAAGACGATGTAACG	587
Db	486	GGATTTAATGTGGCAATGTGGAACCTCCTACGTACGAGCTGTGGCAAGACGATGTAACG	545
Qy	588	GTTTGTACTGTGACAGCTGAAGCTTTACGTTTTGCGAAATACAGAGGGATTTTCGTAC	647
Db	546	GTTTGTACTGTGACAGCTGAAGCTTTACGTTTTGCGAAATACAGAGGGATTTTCGTAC	605
Qy	648	AACACTGATGATCTCAGTGGGCGTTCTTAATGTATGACTGCTGAAGTGTGATCTTAC	707
Db	606	AACACTGATGATCTCAGTGGGCGTTCTTAATGTATGACTGCTGAAGTGTGATCTTAC	665
Qy	708	ATTGAAGCTGGGGAAGGTGTAGTAGGCTCGGCTGACTATCATGGAACAAGCTGTGTCG	767
Db	666	ATTGAAGCTGGGGAAGGTGTAGTAGGCTCGGCTGACTATCATGGAACAAGCTGTGTCG	725
Qy	768	TGTAGGAAGAAATTTCTTTTGAAGACTTAATGCAATTTCTGGAAACGTCGCATTAATACT	827
Db	726	TGTAGGAAGAAATTTCTTTTGAAGACTTAATGCAATTTCTGGAAACGTCGCATTAATACT	785
Qy	828	GAATTTGTCATCATGCAATGCGGAGTTGCCGAATGGCAATCTGATAGATTTCTCTTAT	887
Db	786	GAATTTGTCATCATGCAATGCGGAGTTGCCGAATGGCAATCTGATAGATTTCTCTTAT	845
Qy	888	GTCCTCGGAGATGGAAGAGTCCGTGGGATTAACGCACAATAAATATGTGGGATTCATC	947
Db	846	GTCCTCGGAGATGGAAGAGTCCGTGGGATTAACGCACAATAAATATGTGGGATTCATC	905
Qy	948	CACCTGTGGGGCAATTCGATCGCAGCAATTAATGCACTGG	989
Db	906	CACCTGTGGGGCAATTCGATCGCAGCAATTAATGCACTGG	947

## RESULT 14

ID AAV11400 standard; DNA;. 1389 BP.

AAV11400;

DT 18-AUG-1998 (first entry)

Shiga toxin type 1 gene.

KW Histone-tag; toxoid; antibody; treatment; diagnosis; prevention; Stx;  
KW hemolytic colitis; hemolytic uremic syndrome; ss

**Shigella dysenteriae.**

FH	Key	Location/Qualifiers
1	000	1110

FT	CDS	229.
FT		144.50

```

ET      /product= "Stx1 A subunit"
Em      /note= "No start codon given"

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FT	1120.	.1389
CDS	1120.	.1389
FT	1120.	.1389
FT	1120.	.1389

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FT      /product= "Stx1 B subunit"
yy

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PN W0981.1229-A2.  
YY

PD 19-MAR-1998.  
xy

PF 09-SEP-1997; 97WO-US015836  
YY

PR	10-SEP-1996;	96US-0025637P.
YY		

PA (JACK-) JACKSON FOUND ADVANCEMENT, MILITARY MED  
XX

PI Obrien AB, Schmitt CK; .  
XX

DR WPI; 1998-2073390/18.  
DR P-PSDB: AAW58827. AF

XX	Purification and isolation
PT	

XX vaccines against naemorrhag

PS CLAIM 1; FIG 4; 4/PP; ENGLISH..  
XX

CC the *sluga* (slx) genes (A  
CC peptides. The peptides were hi

Shiga toxins/toxoids and antibodies can be used in the treatment,

CC family. These are associated with haemorrhagic colitis and the life-  
CC diagnosis or prevention of infections mediated by toxins of the sero-  
CC

also useful for the treatment, diagnosis and prevention of disease and

cc  
cc  
XX

infections by pathogenic *Escherichia coli*

[illegible]

	Score	SD	Rank
Query Match	98.3%	0.00	200
Best Local Similarity	99.8%	5.6e-253	

Marlies 800; conservative 0; mismanages 2; needs 0; cups 0

228	GAGAGAAATTACCTTACCTTACCTTCGACCTCGAAGACGATGTAGATTGCTGAAATGTCAT	28
168	TCGCTCTGCAATAGTAGTACTCCATTACAAGACTATTTTCATCAGAGAGTAGCTCTTTACTGAT	227
288	TCCTCTGCAATAGTAGTACTCCATTACAAGACTATTTTCATCAGAGAGTAGCTCTTTACTGAT	347
228	GATTGATAGTGGCAACAGGGGATTAATTTGGTTGGCAATGATGTCACAGAGGATAGATCCAGA	287
348	GATTGATAGTGGCTCAAGGGATTAATTTGGTTGGCAATGATGTCACAGAGGATAGATCCAGA	407
288	GGAAGGCGGTTTAATATATCTACGGCTTATGTGTGAACGAATAATTTAATATGTGACAGG	347

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Db 408 GGAAGCGCGTTTATATATCTACGCTATTGTTGAACGAATATATTATATGTGACAGG 467
Qy 348 ATTCTTAAACAGACAAATATATGTTTTTATTCGCTTCTGATTTTTCACATGTACTT 407
Db 468 ATTCTTAAACAGACAAATATATGTTTTTATTCGCTTCTGATTTTTCACATGTACTT 527
Qy 408 TCCAGGTACACAGCGGTTTACATGTCGTGACAGTAGTATACACAGTACAGCGGT 467
Db 528 TCCAGGTACACAGCGGTTTACATGTCGTGACAGTAGTATACACAGTACAGCGGT 587
Qy 468 TGCAGGATCACTGCTACGCGGATGACATTAATGCCATTGCTTGACTTCTTACT 527
Db 588 TGCAGGATCACTGCTACGCGGATGACATTAATGCCATTGCTTGACTTCTTACT 647
Qy 528 CGATTATATGTCGCTATGTAACCTCACTGACGAGTCTGTGCAAGAGAGTATACG 587
Db 648 GGATTATATGTCGCTATGTAACCTCACTGACGAGTCTGTGCAAGAGAGTATACG 707
Qy 588 GTTGTCTACGACAGCTGAAGCTTTTACGTTTTGCGCAATATACAGAGGATTTCTAC 647
Db 708 GTTGTCTACGACAGCTGAAGCTTTTACGTTTTGCGCAATATACAGAGGATTTCTAC 767
Qy 648 AACACTGATGATCTCAGTGGCGCTTCTTATGTAATGACTGCTGAAGATGTTGATCTTAC 707
Db 768 AACACTGATGATCTCAGTGGCGCTTCTTATGTAATGACTGCTGAAGATGTTGATCTTAC 827
Qy 708 ATTGAACCTGGAAGAGTTGATGAGTCTGCTGCTGATCATATGACACAAAGCTGTTTCG 767
Db 828 ATTGAACCTGGAAGAGTTGATGAGTCTGCTGCTGATCATATGACACAAAGCTGTTTCG 887
Qy 768 TGTAGAGAAATTTCTTTTGGAGCAATATGCAATTTCTGGAAGCGTGGCATTAATACT 827
Db 888 TGTAGAGAAATTTCTTTTGGAGCAATATGCAATTTCTGGAAGCGTGGCATTAATACT 947
Qy 828 GAATTGTCATCATCATGATGCGGAGTTCGCAAGATGCGATCTGATGATGATTTCTTCTAT 887
Db 948 GAATTGTCATCATCATGATGCGGAGTTCGCAAGATGCGATCTGATGATGATTTCTTCTAT 1007
Qy 888 GTGTCCGCGAGATGGAAGATGCGGAGTTCGCAAGATGGAATTAATTTGGGATTTCTATC 947
Db 1008 GTGTCCGCGAGATGGAAGATGCGGAGTTCGCAAGATGGAATTAATTTGGGATTTCTATC 1067
Qy 948 CACTCTGGGGCAATTTCTGATGCGGAGATTAATGAGTATGAGTATGAGTATGAGTATG 989
Db 1068 CACTCTGGGGCAATTTCTGATGCGGAGATTAATGAGTATGAGTATGAGTATGAGTATG 1109

RESULT 15
AAT42673
ID AAT42673 standard; DNA; 980 BP.
XX
AC AAT42673;
XX
DT 26-FEB-1997 (first entry)
XX
DE Flag tag/VT1 A subunit fusion construct.
XX
KW Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine;
KW haemolytic uremic syndrome; detection; ss.
XX
OS Escherichia coli.
XX
FH Key Location/Qualifiers
FT CDS 1..980
FT /tag= a
FT /product= "Flag/VT1 fusion protein"
XX
PN W09630043-A1.
XX
PD 03-OCT-1996.
XX
PF 25-MAR-1996; 96MO-US004093.

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XX 24-MAR-1995; 95US-00410058.
PR (OPHI-) OPHIDIAN PHARM INC.
XX
PA Carrol SB, Stafford DC, Padhye NV;
XX
PI WPI: 1996-505779/50.
DR P-PSDB; AAM06413.
XX
PT Compn. contg. neutralising antitoxin against E.coli vero-toxin - used to
PT treat intoxicated individuals, and as a prophylactic against diarrhoeal
PT disease or extra-intestinal complications of E.coli infection.
XX
PS Example 6; Page 77-78; 101pp; English.
XX
CC Compositions containing neutralising antitoxin against one or more E.
CC coli verotoxin (VT) can be used to treat intoxicated adults and children
CC with enteric bacterial infections. They may also be used as prophylactics
CC e.g. as a vaccine, against diarrhoeal disease or the development of extra
CC -intestinal complications of E.coli infection, especially haemolytic
CC uremic syndrome. The antitoxin can also be used to detect E. coli VT in
CC a sample. The VT is recombinant, preferably a fusion protein containing a
CC non-VT protein sequence and part of the E. coli VT1 or VT2 sequence. This
CC sequence encodes a flag tag/VT1 A subunit fusion protein
XX
SQ Sequence 980 BP; 258 A; 177 C; 250 G; 295 T; 0 U; 0 Other;
XX
Query Match 58.3%; Score 878.4; DB 2; Length 980;
Best Local Similarity 97.2%; Pred. No. 6.1e-253;
Matches 894; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
XX
Qy 70 GCTAAATTCGAACCCGACATGAGACGCCAGATCTGAAGATTTACCTTAGACTTC 129
Db 61 GCTAATCAACAGACAGACAGATGACAGATGATTTCAAGATTTACCTTAGACTTC 120
Qy 130 TCGACTGCAAGACGATATGATTCCTGATATCTATCTGCTATGATATGATCTCA 189
Db 121 TCGACTGCAAGACGATATGATTCCTGATATCTATCTGCTATGATATGATCTCA 180
Qy 190 TTAGAGACTATTTATAGAGGATGATCTTACTGATGATGATGATGATGATGATGAT 249
Db 181 TTAGAGACTATTTATAGAGGATGATCTTACTGATGATGATGATGATGATGATGAT 240
Qy 250 AATTTGTTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 309
Db 241 AATTTGTTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Qy 310 CGGCTTATTTGTAACGAATATTTATATGATGACAGATTTGTTTACAGACAAATAT 369
Db 301 CGGCTTATTTGTAACGAATATTTATATGATGACAGATTTGTTTACAGACAAATAT 360
Qy 370 GTTTTATATGCTTGTGATTTTTCACATGATTTTTCAGGATGATGATGATGATGAT 429
Db 361 GTTTTATATGCTTGTGATTTTTCACATGATTTTTCAGGATGATGATGATGATGAT 420
Qy 430 TTGTCTGATGACAGTATATACAGCGTATACAGCGTGTGAGGAGATGATGATGAT 489
Db 421 TTGTCTGATGACAGTATATACAGCGTATACAGCGTGTGAGGAGATGATGATGAT 480
Qy 490 ATGCAATATATGCGCATCTGTTGATCTATCTGATGATGATGATGATGATGATGAT 549
Db 481 ATGCAATATATGCGCATCTGTTGATCTATCTGATGATGATGATGATGATGATGAT 540
Qy 550 AACTCAGTACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 609
Db 541 AACTCAGTACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Qy 610 GCTTTACGTTTTTGGCAATATCAAGAGGATTTGATCAACACATGATGATGATGAT 669
Db 601 GCTTTACGTTTTTGGCAATATCAAGAGGATTTGATCAACACATGATGATGATGAT 660
Qy 670 GCTTTATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729

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Db      661 |||||CGTTCTTATGTATGACTGCTGAAGATGTTGATCTTACATGAACTGGGGAAGTTGAGT 720
QY      730 AGGTCCTGCGCTGACTATCATGTGACAAGACTCTGTTGCGTAGAAGAAATTTCTTTGGA 789
Db      721 AGGTCCTGCGCTGACTATCATGTGACAAGACTCTGTTGCGTAGAAGAAATTTCTTTGGA 780
QY      790 AGCATTAAATGCAATTTCTGGGAAGCGTGCGCATTAATGCTGAATTTGTCATCATGATGATCG 849
Db      781 AGCATTAAATGCAATTTCTGGGAAGCGTGCGCATTAATGCTGAATTTGTCATCATGATGATCG 840
QY      850 CGAGTTGCCAGAAATGGCATCTGATGAGTTTCTTCTATGTGTCCGCGAGATGGAAGATC 909
Db      841 CGAGTTGCCAGAAATGGCATCTGATGAGTTTCTTCTATGTGTCCGCGAGATGGAAGATC 900
QY      910 CGTGGGATTACGACATAATAATATTGTGGGATTCACTCGTGGGGCAATTCGATG 969
Db      901 CGTGGGATTACGACATAATAATATTGTGGGATTCACTCGTGGGGCAATTCGATG 960
QY      970 CGCAGAACTATTAGCAGTGG 989
Db      961 CGCAGAACTATTAGCAGTGG 980
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Search completed: January 23, 2007, 01:37:36  
job time : 1025 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 23:31:07 ; Search time 1144 Seconds  
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3837.437 Million cell updates/sec

Title: US-10-765-580-11

Perfect score: 1507

Sequence: 1 atgacacatcatcatcatca.....gtgacagcgagcggtga 1507

Scoring table: IDENTITY NUC

Searched: 3950299 seqs, 1456545396 residues

Total number of hits satisfying chosen parameters: 7900598

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	875.8	58.1	948	US-11-177-646-413	Sequence 413, Appl
2	498.4	33.1	502	US-11-136-524-93	Sequence 93, Appl
3	498	33.0	576	US-11-021-541-2	Sequence 2, Appl
4	498	33.0	576	US-11-422-932-3	Sequence 3, Appl
5	498	33.0	576	US-11-422-947-3	Sequence 3, Appl
6	498	33.0	576	US-11-423-006-3	Sequence 3, Appl
7	498	33.0	576	US-11-370-301-11	Sequence 11, Appl
8	498	33.0	576	US-11-370-301-11	Sequence 11, Appl
9	498	33.0	610	US-10-948-737-13223	Sequence 13223, A
10	498	33.0	649	US-10-473-173-60	Sequence 60, Appl
11	498	33.0	658	US-11-282-283-3	Sequence 3, Appl
12	498	33.0	990	US-11-320-422-36	Sequence 36, Appl
13	498	33.0	990	US-11-346-596-3	Sequence 3, Appl
14	498	33.0	3542	US-11-349-727-9	Sequence 9, Appl
15	496.4	32.9	990	US-11-376-990-3	Sequence 3, Appl
16	494.8	32.8	3166	US-10-553-520-98	Sequence 98, Appl
17	494.8	32.8	3166	US-11-359-721-12	Sequence 12, Appl
18	494.8	32.8	3166	US-11-347-748-12	Sequence 12, Appl
19	441.2	29.3	541	US-11-266-748A-59044	Sequence 59044, A
20	441.2	29.3	600	US-10-956-160-2866	Sequence 2866, Ap
21	441.2	29.3	600	US-10-956-160-212973	Sequence 212973, A
22	416	27.6	648	US-11-021-541-3	Sequence 3, Appl

23	416	27.6	648	7	US-11-422-932-4	Sequence 4, Appl
24	416	27.6	648	7	US-11-422-947-4	Sequence 4, Appl
25	416	27.6	648	7	US-11-423-006-4	Sequence 4, Appl
26	416	27.6	1723	8	US-11-414-724-47	Sequence 47, Appl
27	416	27.6	1723	8	US-11-266-748A-29382	Sequence 29382, A
28	416	27.6	1723	10	US-11-339-733-61	Sequence 61, Appl
29	416	27.6	3614	7	US-11-349-727-11	Sequence 11, Appl
30	407.2	27.0	972	10	US-11-361-977A-61	Sequence 61, Appl
31	406	26.9	2848	9	US-11-320-422-42	Sequence 42, Appl
32	405.4	26.9	978	10	US-11-361-977A-62	Sequence 62, Appl
33	405	26.9	744	10	US-11-361-977A-64	Sequence 64, Appl
34	405	26.9	963	10	US-11-361-977A-58	Sequence 58, Appl
35	405	26.9	978	10	US-11-361-977A-52	Sequence 52, Appl
36	405	26.9	978	10	US-11-361-977A-55	Sequence 55, Appl
37	403.2	26.8	750	10	US-11-361-977A-65	Sequence 65, Appl
38	403.2	26.8	969	10	US-11-361-977A-59	Sequence 59, Appl
39	403.2	26.8	984	10	US-11-361-977A-53	Sequence 53, Appl
40	403.2	26.8	984	10	US-11-361-977A-56	Sequence 56, Appl
41	377.2	25.0	600	6	US-10-956-160-212974	Sequence 212974,
42	377.2	25.0	654	6	US-10-956-160-2867	Sequence 2867, Ap
43	365	24.2	3665	7	US-11-349-727-13	Sequence 13, Appl
44	365	24.2	3665	9	US-11-323-964-25	Sequence 25, Appl
45	365	24.2	3665	9	US-11-323-964-43	Sequence 43, Appl

## ALIGNMENTS

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RESULT 1
US-11-177-646-413
; Sequence 413, Application US/11177646
; Publication No. US20060210967A1
; GENERAL INFORMATION:
; APPLICANT: AGAN, BRIAN
; APPLICANT: ROWLEY, ROBB
; APPLICANT: SETO, DONALD
; APPLICANT: STENGER, DAVID
; APPLICANT: THORNTON, JENNIFER
; APPLICANT: TIBBETTS, CLARK
; APPLICANT: THACH, DZUNG
; APPLICANT: TORCH, GARY
; APPLICANT: WALTER, ELIZABETH
; APPLICANT: WANG, ZHENG
; TITLE OF INVENTION: RE-SEQUENCING PATHOGEN MICROARRAY
; FILE REFERENCE: AFD 735
; CURRENT APPLICATION NUMBER: US/11/177, 646
; PRIOR FILING DATE: 2005-07-02
; PRIOR APPLICATION NUMBER: 60/590931
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 413
; LENGTH: 948
; TYPE: DNA
; ORGANISM: E. coli 0157:H7, 32400301.1-948
US-11-177-646-413

Query Match      58.1%; Score 875.8; DB 10; Length 948;
Best Local Similarity 99.2%; Pred. No. 4.5e-270;
Matches 880; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      103 GATCTGAAGAAATTACCTTTCGACTGCAAGCAAGCAATGATGATTCGCTGAAT 162
      |||
DB      61 GTTCGAAGAAATTACCTTTCGACTGCAAGCAAGCAATGATGATTCGCTGAAT 120

QY      163 GTCTTCGCTTCGAAATGAGTACCTTCAGACTATTCATCAGAGGAGTACCTTTA 222
      |||
DB      121 GTCTTCGCTTCGAAATGAGTACCTTCAGACTATTCATCAGAGGAGTACCTTTA 180

QY      223 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 282
      |||
DB      181 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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QY 283 CCAGAGGAGGAGGGGTTTAAATCTACGCGCTTATGTTGAACGAATAATTAATATGTC 342
DB 241 CCAGAGGAGGAGGGGTTTAAATCTACGCGCTTATGTTGAACGAATAATTAATATGTC 300
QY 343 ACAGGATTTGTTAACAGGACAAATATATGTTTATGCTTGGCTGATTTTCAATGTT 402
DB 301 ACAGGATTTGTTAACAGGACAAATATATGTTTATGCTTGGCTGATTTTCAATGTT 360
QY 403 ACCCTTCAGATGACACAGCGGTTTACATGTCGTGTGACAGTACGCTATACAGGTTACAG 462
DB 361 ACCCTTCAGATGACACAGCGGTTTACATGTCGTGTGACAGTACGCTATACAGGTTACAG 420
QY 463 CGTGTTCAGAGGATCACTGCTGACGCGGATGCAATTAATGCCATTGCTTACTTCTT 522
DB 421 CGTGTTCAGAGGATCACTGCTGACGCGGATGCAATTAATGCCATTGCTTACTTCTT 480
QY 523 TATCTGATTTTAAATGTCGATAGTGAACCTCAGCTGACGAGTCTGTGGCAAGGAGT 582
DB 481 TATCTGATTTTAAATGTCGATAGTGAACCTCAGCTGACGAGTCTGTGGCAAGGAGT 540
QY 583 TTAAGGTTTGTACTGTCGACGCTGAAGCTTTACGTTTTCGGCAATAACAGAGGGGATT 642
DB 541 TTAAGGTTTGTACTGTCGACGCTGAAGCTTTACGTTTTCGGCAATAACAGAGGGGATT 600
QY 643 CGTACAACTGATGATGCTCACTGAGGCGTTTCTTATGTAATGACTGCTGAAGTGTGAT 702
DB 601 CGTACAACTGATGATGCTCACTGAGGCGTTTCTTATGTAATGACTGCTGAAGTGTGAT 660
QY 703 CTTCACATGTAACGCGGGAAGGTTGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 762
DB 661 CTTCACATGTAACGCGGGAAGGTTGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 763 GTTCTGTAGAGAAATTTCTTTTGAAGCAATTAATCAATCTGGGACGCTGCTGCTGCT 822
DB 721 GTTCTGTAGAGAAATTTCTTTTGAAGCAATTAATCAATCTGGGACGCTGCTGCTGCTG 780
QY 823 ATACTGATTTGCTATCATCATGCAATCGCGAGTTGCCGAATGCGATCTGATGAGTTCT 882
DB 781 ATACTGATTTGCTATCATCATGCAATCGCGAGTTGCCGAATGCGATCTGATGAGTTCT 840
QY 883 TCTATGTCGCGGAGATGGAAGTCCGCGGATTCGCAATTAATTAATTAATTAATTAATTA 942
DB 841 TCTATGTCGCGGAGATGGAAGTCCGCGGATTCGCAATTAATTAATTAATTAATTAATTA 900
QY 943 TCAATCCACTCTGGGGGCAATTTCTGATGCGGAGAACTTTAGCAAGTGG 989
DB 901 TCAATCCACTCTGGGGGCAATTTCTGATGCGGAGAACTTTAGCAAGTGG 947
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## RESULT 2

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US-11-136-524-93
; Sequence 93, Application US/11136524
; Publication No. US20060094034A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Josee
; APPLICANT: BEKAL, Sadja
; TITLE OF INVENTION: ARRAY AND USES THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/11/136,524
; CURRENT FILING DATE: 2005-05-25
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-136-524-93
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Query Match 33.1%; Score 498.4; DB 8; Length 502;  
Best Local Similarity 99.8%; Pred. No. 4,7e-149;  
Matches 499; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 108 GAAGAAATTTTACCTTAGACTTCTCGACTGCAAGACGATAGTAGATTCGCTGAATGTCAT 167
DB 3 GAAGAAATTTTACCTTAGACTTCTCGACTGCAAGACGATAGTAGATTCGCTGAATGTCAT 62
QY 168 TGGCTCTGCAATAGTACTTCCATTACAGCTATTTTCAATGAGAGGTACTCTTACTGAT 227
DB 63 TGGCTCTGCAATAGTACTTCCATTACAGCTATTTTCAATGAGAGGTACTCTTACTGAT 122
QY 228 GATTATAGTGGCACAGGGGATTAATTTTTCAGTTGATGTCAGAGGATAGATTCAGA 287
DB 123 GATTATAGTGGCTCAGGGGATTAATTTTTCAGTTGATGTCAGAGGATAGATTCAGA 182
QY 288 GGAAGGCGGTTTAAATCTACGCGCTTATGTTGAAAGCAATTAATTAATTAATTAAT 347
DB 183 GGAAGGCGGTTTAAATCTACGCGCTTATGTTGAAAGCAATTAATTAATTAATTAAT 242
QY 348 ATTTGTTAAACAGACAAATTAATGTTTATGCTTGTGATTTTTCATGTTTACCTT 407
DB 243 ATTTGTTAAACAGACAAATTAATGTTTATGCTTGTGATTTTTCATGTTTACCTT 302
QY 408 TCCAGGTACACAGCGGTTTACATTTGCTGTGACAGTACTATACAGCTTACAGCGTGT 467
DB 303 TCCAGGTACACACGCGTTTACATTTGCTGTGACAGTACTATACAGCTTACAGCGTGT 362
QY 468 TCCAGGATCACTGCTGATCGGGATGCAATTAATGSCCATTTGCTGACTTCTTATCT 527
DB 363 TCCAGGATCACTGCTGATCGGGATGCAATTAATGSCCATTTGCTGACTTCTTATCT 422
QY 528 GGATTTAATGTCGATAGTGAACCTCACTGACGAGTGTGGCAAGCGGATGTTAG 587
DB 423 GGATTTAATGTCGATAGTGAACCTCACTGACGAGTGTGGCAAGCGGATGTTAG 482
QY 588 GTTGTACTGTGACAGCTG 607
DB 483 GTTGTACTGTGACAGCTG 502
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## RESULT 3

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US-11-021-541-2
; Sequence 2, Application US/11021541
; Publication No. US20060287259A1
; GENERAL INFORMATION:
; APPLICANT: REICH, SAMUEL JOTHAM
; APPLICANT: TOLENTINO, MICHAEL J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE
; FILE REFERENCE: DBR-04-1324R
; CURRENT APPLICATION NUMBER: US/11/021,541
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,099
; NUMBER OF SEQ ID NOS: 1733
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-021-541-2
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Query Match 33.0%; Score 498; DB 7; Length 576;  
Best Local Similarity 100.0%; Pred. No. 6,9e-149;  
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1010 GCACCCATGCGACAGAGAGGAGGCAATCATCAGAAAGTGTGAAGTTCAATGATGTC 1069
DB 79 GCACCCATGCGACAGAGAGGAGGCAATCATCAGAAAGTGTGAAGTTCAATGATGTC 138
QY 1070 TATCAGCGAGCTACCTGATCCATTCATGAGACCTCTGTGGACATCTTCCAGAGTACCT 1129
DB 139 TATCAGCGAGCTACCTGATCCATTCATGAGACCTCTGTGGACATCTTCCAGAGTACCT 198
QY 1130 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCCCTGATGCGATGCGGGGCTGC 1189
DB 199 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCCCTGATGCGATGCGGGGCTGC 258
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QY 1190 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGTCCAAATCATCATGAGATT 1249  
DB 259 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGTCCAAATCATCATGAGATT 318  
QY 1250 ATGCGGATCAAACTTCACCAAGGCCAGCATATGAGAGATGAGTCTTCTCAGACAAC 1309  
DB 319 ATGCGGATCAAACTTCACCAAGGCCAGCATATGAGAGATGAGTCTTCTCAGACAAC 378  
QY 1310 AATGTGAATGACGACCAAGAAAGATGAGCAAGCAAGAAATCCCTGTGGGCGCTTGC 1369  
DB 379 AATGTGAATGACGACCAAGAAAGATGAGCAAGCAAGAAATCCCTGTGGGCGCTTGC 438  
QY 1370 TCAGAGCGGAGAAAGCATTTGTTGTACAAAGATCCGACAGCTGTAAATGTTCTTCAAA 1429  
DB 439 TCAGAGCGGAGAAAGCATTTGTTGTACAAAGATCCGACAGCTGTAAATGTTCTTCAAA 498  
QY 1430 AACACGACTCCGCTTGCAAGCGAGCGAGCTTGAGTTAAACGACGTAATTGACAGATGT 1489  
DB 499 AACACGACTCCGCTTGCAAGCGAGCGAGCTTGAGTTAAACGACGTAATTGACAGATGT 558  
QY 1490 GACAGCGGAGCGGTGA 1507  
DB 559 GACAGCGGAGCGGTGA 576

## RESULT 4

US-11-422-932-3  
; Sequence 3, Application US/11422932  
; Publication No. US20060286073A1  
; GENERAL INFORMATION:  
; APPLICANT: Tolentino, Michael J.  
; APPLICANT: Reich, Samuel Jotham  
; TITLE OF INVENTION: Compositions and Methods for siRNA  
; FILE REFERENCE: 43826-1  
; CURRENT APPLICATION NUMBER: US/11/422,932  
; CURRENT FILING DATE: 2006-06-08  
; PRIOR APPLICATION NUMBER: US/10/294,228  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: US 60/398,417  
; PRIOR FILING DATE: 2002-07-24  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 576  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-422-932-3

Query Match 33.0%; Score 498; DB 7; Length 576;  
Best Local Similarity 100.0%; Pred. No. 6.9e-149;  
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCCATGCGAGAGAGAGAGAGAGATCATCATGAGAGTGTGATGATGTC 1069  
DB 79 GCACCCATGCGAGAGAGAGAGAGAGATCATCATGAGAGTGTGATGATGTC 138  
QY 1070 TATCAGCGGAGCTACTGCGCATCATCGAGACCTGTGAGATCTTCCAGAGTAACCT 1129  
DB 139 TATCAGCGGAGCTACTGCGCATCATCGAGACCTGTGAGATCTTCCAGAGTAACCT 198  
QY 1130 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTGATGAGATGCGGGGCTGC 1189  
DB 199 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTGATGAGATGCGGGGCTGC 258  
QY 1199 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGATCCAAATCATCATGAGATT 1249  
DB 259 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGATCCAAATCATCATGAGATT 318  
QY 1250 ATGCGGATCAAACTTCACCAAGGCCAGCATATGAGAGATGAGTCTTCTCAGACAAC 1309  
DB 319 ATGCGGATCAAACTTCACCAAGGCCAGCATATGAGAGATGAGTCTTCTCAGACAAC 378

QY 1310 AATGTGAATGACGACCAAGAAAGATGAGCAAGCAAGAAATCCCTGTGGGCGCTTGC 1369  
DB 379 AATGTGAATGACGACCAAGAAAGATGAGCAAGCAAGAAATCCCTGTGGGCGCTTGC 438  
QY 1370 TCAGAGCGGAGAAAGCATTTGTTGTACAAAGATCCGACAGCTGTAAATGTTCTTCAAA 1429  
DB 439 TCAGAGCGGAGAAAGCATTTGTTGTACAAAGATCCGACAGCTGTAAATGTTCTTCAAA 498  
QY 1430 AACACGACTCCGCTTGCAAGCGAGCGAGCTTGAGTTAAACGACGTAATTGACAGATGT 1489  
DB 499 AACACGACTCCGCTTGCAAGCGAGCGAGCTTGAGTTAAACGACGTAATTGACAGATGT 558  
QY 1490 GACAGCGGAGCGGTGA 1507  
DB 559 GACAGCGGAGCGGTGA 576

## RESULT 5

US-11-422-947-3  
; Sequence 3, Application US/11422947  
; Publication No. US20060292120A1  
; GENERAL INFORMATION:  
; APPLICANT: Tolentino, Michael J.  
; APPLICANT: Reich, Samuel Jotham  
; TITLE OF INVENTION: Compositions and Methods for siRNA  
; FILE REFERENCE: 43826-1  
; CURRENT APPLICATION NUMBER: US/11/422,947  
; CURRENT FILING DATE: 2006-06-08  
; PRIOR APPLICATION NUMBER: US/10/294,228  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: US 60/398,417  
; PRIOR FILING DATE: 2002-07-24  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 576  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-422-947-3

Query Match 33.0%; Score 498; DB 7; Length 576;  
Best Local Similarity 100.0%; Pred. No. 6.9e-149;  
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCCATGCGAGAGAGAGAGAGAGATCATCATGAGAGTGTGATGATGTC 1069  
DB 79 GCACCCATGCGAGAGAGAGAGAGAGATCATCATGAGAGTGTGATGATGTC 138  
QY 1070 TATCAGCGGAGCTACTGCGCATCATCGAGACCTGTGAGATCTTCCAGAGTAACCT 1129  
DB 139 TATCAGCGGAGCTACTGCGCATCATCGAGACCTGTGAGATCTTCCAGAGTAACCT 198  
QY 1130 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTGATGAGATGCGGGGCTGC 1189  
DB 199 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTGATGAGATGCGGGGCTGC 258  
QY 1199 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGATCCAAATCATCATGAGATT 1249  
DB 259 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGATCCAAATCATCATGAGATT 318  
QY 1250 ATGCGGATCAAACTTCACCAAGGCCAGCATATGAGAGATGAGTCTTCTCAGACAAC 1309  
DB 319 ATGCGGATCAAACTTCACCAAGGCCAGCATATGAGAGATGAGTCTTCTCAGACAAC 378  
QY 1310 AATGTGAATGACGACCAAGAAAGATGAGCAAGCAAGAAATCCCTGTGGGCGCTTGC 1369  
DB 379 AATGTGAATGACGACCAAGAAAGATGAGCAAGCAAGAAATCCCTGTGGGCGCTTGC 438  
QY 1370 TCAGAGCGGAGAAAGCATTTGTTGTACAAAGATCCGACAGCTGTAAATGTTCTTCAAA 1429  
DB 439 TCAGAGCGGAGAAAGCATTTGTTGTACAAAGATCCGACAGCTGTAAATGTTCTTCAAA 498







Db 496 AACACAGACTCGCGTTCGCAAGCGGAGGAGGAGCTTGAGTTAAACGAAGTACTTGACAGATGT 555  
 QY 1490 GACACAGCCGAGGCGGCTGA 1507  
 Db 556 GACACAGCCGAGGCGGCTGA 573

## RESULT 10

US-10-473-173-60  
 ; Sequence 60, Application US/10473173  
 ; Publication No. US200608823A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN ANDEL INSTITUTE  
 ; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell  
 ; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification  
 ; FILE REFERENCE: 38345-170094  
 ; CURRENT APPLICATION NUMBER: US/10/473,173  
 ; PRIOR FILING DATE: 2003-09-29  
 ; PRIOR APPLICATION NUMBER: US 60/279,411  
 ; NUMBER OF SEQ ID NOS: 498  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 60  
 ; LENGTH: 649  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-473-173-60

Query Match 33.0%; Score 498; DB 6; Length 649;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-149;  
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCAACCATGCGACAGAGAGGAGGAGATCATCAGAACTGGTGAAGTTTCATGATGTC 1069  
 Db 95 GCACCCATGCGACAGAGAGGAGGAGATCATCAGAACTGGTGAAGTTTCATGATGTC 154  
 QY 1070 TATCAGCGCAGTACTGCTCCATCCATCGAGACCCCTGTGTGACATCTTCCAGAGTACCT 1129  
 Db 155 TATCAGCGCAGTACTGCTCCATCCATCGAGACCCCTGTGTGACATCTTCCAGAGTACCT 214  
 QY 1130 GATGAGATCGAGTACATCTTCCATCCATCGAGACCCCTGTGTGACATCTTCCAGAGTACCT 1189  
 Db 215 GATGAGATCGAGTACATCTTCCATCCATCGAGACCCCTGTGTGACATCTTCCAGAGTACCT 274  
 QY 1190 TGCAGATGCGAGGCGCTGTGAGTGTGTCCTCAGAGAGTCCAAATCACCATGACAGTT 1249  
 Db 275 TGCAGATGCGAGGCGCTGTGAGTGTGTCCTCAGAGAGTCCAAATCACCATGACAGTT 334  
 QY 1250 ATGCGGATCAAACTCTCAACAGGCGAGACATAGAGAGATGAGCTTCTTACAGCACAC 1309  
 Db 335 ATGCGGATCAAACTCTCAACAGGCGAGACATAGAGAGATGAGCTTCTTACAGCACAC 394  
 QY 1310 AAATGTGAATGCGACACCAAGAAAGATAGAGCAAGAAAGAAATCCCTGTGGGCTTGC 1369  
 Db 395 AAATGTGAATGCGACACCAAGAAAGATAGAGCAAGAAAGAAATCCCTGTGGGCTTGC 454  
 QY 1370 TCAGAGCGGAGAAAGCATTTGTTGTACAAGATCCGAGACGTGTAAATGTTCTCTGAAA 1429  
 Db 455 TCAGAGCGGAGAAAGCATTTGTTGTACAAGATCCGAGACGTGTAAATGTTCTCTGAAA 514  
 QY 1430 AACACAGACTCGCGTTCGCAAGCGGAGGAGCTTGAGTTAAACGAAGTACTTGACAGTGT 1489  
 Db 515 AACACAGACTCGCGTTCGCAAGCGGAGGAGCTTGAGTTAAACGAAGTACTTGACAGTGT 574  
 QY 1490 GACACAGCCGAGGCGGCTGA 1507  
 Db 575 GACACAGCCGAGGCGGCTGA 592

RESULT 11  
 US-11-282-283-3  
 ; Sequence 3, Application US/11282283

; Publication No. US20060141627A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Comer, Allen  
 ; TITLE OF INVENTION: Vectors for Stable Gene Expression  
 ; FILE REFERENCE: STRATA-10492  
 ; CURRENT APPLICATION NUMBER: US/11/282,283  
 ; CURRENT FILING DATE: 2005-11-18  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 3  
 ; LENGTH: 658  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-11-282-283-3

Query Match 33.0%; Score 498; DB 9; Length 658;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-149;  
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCAACCATGCGACAGAGAGGAGGAGATCATCAGAACTGGTGAAGTTTCATGATGTC 1069  
 Db 81 GCACCCATGCGACAGAGAGGAGGAGATCATCAGAACTGGTGAAGTTTCATGATGTC 140  
 QY 1070 TATCAGCGCAGTACTGCTCCATCCATCGAGACCCCTGTGTGACATCTTCCAGAGTACCT 1129  
 Db 141 TATCAGCGCAGTACTGCTCCATCCATCGAGACCCCTGTGTGACATCTTCCAGAGTACCT 200  
 QY 1130 GATGAGATCGAGTACATCTTCCATCCATCGAGACCCCTGTGTGACATCTTCCAGAGTACCT 1189  
 Db 201 GATGAGATCGAGTACATCTTCCATCCATCGAGACCCCTGTGTGACATCTTCCAGAGTACCT 260  
 QY 1190 TGCAGATGCGAGGCGCTGTGAGTGTGTCCTCAGAGAGTCCAAATCACCATGACAGTT 1249  
 Db 261 TGCAGATGCGAGGCGCTGTGAGTGTGTCCTCAGAGAGTCCAAATCACCATGACAGTT 320  
 QY 1250 ATGCGGATCAAACTCTCAACAGGCGAGACATAGAGAGATGAGCTTCTTACAGCACAC 1309  
 Db 321 ATGCGGATCAAACTCTCAACAGGCGAGACATAGAGAGATGAGCTTCTTACAGCACAC 380  
 QY 1310 AAATGTGAATGCGACACCAAGAAAGATAGAGCAAGAAAGAAATCCCTGTGGGCTTGC 1369  
 Db 381 AAATGTGAATGCGACACCAAGAAAGATAGAGCAAGAAAGAAATCCCTGTGGGCTTGC 440  
 QY 1370 TCAGAGCGGAGAAAGCATTTGTTGTACAAGATCCGAGACGTGTAAATGTTCTCTGAAA 1429  
 Db 441 TCAGAGCGGAGAAAGCATTTGTTGTACAAGATCCGAGACGTGTAAATGTTCTCTGAAA 500  
 QY 1430 AACACAGACTCGCGTTCGCAAGCGGAGGAGCTTGAGTTAAACGAAGTACTTGACAGTGT 1489  
 Db 501 AACACAGACTCGCGTTCGCAAGCGGAGGAGCTTGAGTTAAACGAAGTACTTGACAGTGT 560  
 QY 1490 GACACAGCCGAGGCGGCTGA 1507  
 Db 561 GACACAGCCGAGGCGGCTGA 578

## RESULT 12

US-11-320-422-36  
 ; Sequence 36, Application US/11320422  
 ; Publication No. US20060154285A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Leung, Tinchung  
 ; APPLICANT: Robishaw, Janet D.  
 ; TITLE OF INVENTION: Zebrafish Heterotrimer G-Protein Gamma 2 Subunit (GN2)  
 ; FILE REFERENCE: GEIS-0014  
 ; CURRENT APPLICATION NUMBER: US/11/320,422  
 ; CURRENT FILING DATE: 2005-12-28  
 ; PRIOR APPLICATION NUMBER: US 60/640,802  
 ; PRIOR FILING DATE: 2004-12-29  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 36  
 ; LENGTH: 990

TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-320-422-36

Query Match 33.0%; Score 498; DB 9; Length 990;  
Best Local Similarity 100.0%; Pred. No. 9.9e-149;  
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1010 GCACCCATGGCAGAGAGAGAGAGAGATCATCAGAAATGTGAGTTCATGATGTC 1069  
135 GCACCCATGGCAGAGAGAGAGAGATCATCAGAAATGTGAGTTCATGATGTC 194  
1070 TATCAGCGAGCTACTGCTCATTCATCGAGACCTGTGTGACATCTTCCAGAGTACCT 1129  
195 TATCAGCGAGCTACTGCTCATTCATCGAGACCTGTGTGACATCTTCCAGAGTACCT 254  
1130 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCTGCTGATGCTGAGTTC 1189  
255 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCTGCTGATGCTGAGTTC 314  
1190 TGCAATGACGAGGCTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1249  
315 TGCAATGACGAGGCTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 374  
1250 ATGCGATCAAACTCTCACCAGGCGCAGCAGATAGAGAGATGAGCTTCTACAGCAAC 1309  
375 ATGCGATCAAACTCTCACCAGGCGCAGCAGATAGAGAGATGAGCTTCTACAGCAAC 434  
1310 AAATGTGAATGACAGCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1369  
435 AAATGTGAATGACAGCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 494  
1370 TCAGAGCGAG 1429  
495 TCAGAGCGAG 554  
1430 AACACAGACTGCGCTTGCAAGGCGAGGAGCTTGAAGTAAAGTAAAGTAAAGTAA 1489  
555 AACACAGACTGCGCTTGCAAGGCGAGGAGCTTGAAGTAAAGTAAAGTAAAGTAA 614  
1490 GACAAGCCGAGGCGGTGA 1507  
615 GACAAGCCGAGGCGGTGA 632

## RESULT 13

US-11-346-596-3  
Sequence 3, Application US/11346596  
Publication No. US20060188503A1  
GENERAL INFORMATION:  
APPLICANT: Shen, Ben-Quan  
APPLICANT: Zionscheck, Thomas  
TITLE OF INVENTION: MODULATION OF ENOS ACTIVITY AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P17351  
CURRENT APPLICATION NUMBER: US/11/346,596  
CURRENT FILING DATE: 2006-02-02  
PRIOR APPLICATION NUMBER: US/09/700,806  
PRIOR FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: PCT/US00/30294  
PRIOR FILING DATE: 2000-11-02  
PRIOR APPLICATION NUMBER: US 60/163,132  
PRIOR FILING DATE: 1999-11-02  
NUMBER OF SEQ ID NOS: 4  
SEQ ID NO 3  
LENGTH: 990  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-346-596-3

Query Match 33.0%; Score 498; DB 10; Length 990;  
Best Local Similarity 100.0%; Pred. No. 9.9e-149;  
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1010 GCACCCATGGCAGAGAGAGAGAGAGATCATCAGAAATGTGAGTTCATGATGTC 1069  
135 GCACCCATGGCAGAGAGAGAGAGAGATCATCAGAAATGTGAGTTCATGATGTC 194  
1070 TATCAGCGAGCTACTGCTCATTCATCGAGACCTGTGTGACATCTTCCAGAGTACCT 1129  
195 TATCAGCGAGCTACTGCTCATTCATCGAGACCTGTGTGACATCTTCCAGAGTACCT 254  
1130 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCTGCTGATGCTGAGTTC 1189  
255 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCTGCTGATGCTGAGTTC 314  
1190 TGCAATGACGAGGCTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1249  
315 TGCAATGACGAGGCTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 374  
1250 ATGCGATCAAACTCTCACCAGGCGCAGCAGATAGAGAGATGAGCTTCTACAGCAAC 1309  
375 ATGCGATCAAACTCTCACCAGGCGCAGCAGATAGAGAGATGAGCTTCTACAGCAAC 434  
1310 AAATGTGAATGACAGCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1369  
435 AAATGTGAATGACAGCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 494  
1370 TCAGAGCGAG 1429  
495 TCAGAGCGAG 554  
1430 AACACAGACTGCGCTTGCAAGGCGAGGAGCTTGAAGTAAAGTAAAGTAAAGTAA 1489  
555 AACACAGACTGCGCTTGCAAGGCGAGGAGCTTGAAGTAAAGTAAAGTAAAGTAA 614  
1490 GACAAGCCGAGGCGGTGA 1507  
615 GACAAGCCGAGGCGGTGA 632

## RESULT 14

US-11-349-727-9  
Sequence 9, Application US/11349727  
Publication No. US2007009484A1  
GENERAL INFORMATION:  
APPLICANT: HUNT, KELLY K.  
APPLICANT: SUH, YOUNG-JIN  
APPLICANT: SWISHER, STEPHEN G.  
APPLICANT: PATNER, ABUTJANG  
APPLICANT: RAMESH, RAJAGOPAL  
APPLICANT: SHANKER, MANISH  
TITLE OF INVENTION: COMPOSITIONS AND METHODS INVOLVING MDA-7 FOR THE  
TREATMENT OF CANCER  
FILE REFERENCE: UTSC:924US/INGN:1330US  
CURRENT APPLICATION NUMBER: US/11/349,727  
CURRENT FILING DATE: 2006-02-08  
PRIOR APPLICATION NUMBER: 60/650,807  
PRIOR FILING DATE: 2005-02-08  
PRIOR APPLICATION NUMBER: 60/661,679  
PRIOR FILING DATE: 2005-03-14  
PRIOR APPLICATION NUMBER: 60/676,096  
PRIOR FILING DATE: 2005-04-29  
PRIOR APPLICATION NUMBER: 60/749,372  
PRIOR FILING DATE: 2005-12-12  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 9  
LENGTH: 3542  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-349-727-9

Query Match 33.0%; Score 498; DB 7; Length 3542;  
Best Local Similarity 100.0%; Pred. No. 2.3e-148;  
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCATGCGAGAGAGAGGAGGAGAAATCATCAGAAATGAGTGAATTCATGATGTC 1069  
DB 1110 GCACCATGCGAGAGAGAGGAGGAGAAATCATCAGAAATGAGTGAATTCATGATGTC 1169  
QY 1070 TATCAGCGGAGTACTGCTCCATTCAGATGAGACCTGTGTGACATCTTCCAGAGATACCTT 1129  
DB 1170 TATCAGCGGAGTACTGCTCCATTCAGATGAGACCTGTGTGACATCTTCCAGAGATACCTT 1229  
QY 1130 GATGAGATGAGATGATCTTCAAGCCTGTGTGACATCTTCCAGAGATGAGTGTG 1189  
DB 1230 GATGAGATGAGATGATCTTCAAGCCTGTGTGACATCTTCCAGAGATGAGTGTG 1289  
QY 1190 TGCATGAGAGAGGAGGAGTGTGTGCTGAGAGATGAGATGAGATGAGATGAGATG 1249  
DB 1290 TGCATGAGAGAGGAGGAGTGTGTGCTGAGAGATGAGATGAGATGAGATGAGATG 1349  
QY 1250 ATGCGGATCAAACTTCAACGAGGAGGAGATGAGATGAGATGAGATGAGATGAGATG 1309  
DB 1350 ATGCGGATCAAACTTCAACGAGGAGGAGATGAGATGAGATGAGATGAGATGAGATG 1409  
QY 1310 AAATGTGAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1369  
DB 1410 AAATGTGAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1469  
QY 1370 TCAGAGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1429  
DB 1470 TCAGAGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1529  
QY 1430 AACACAGACTGCGGTTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1489  
DB 1530 AACACAGACTGCGGTTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1589  
QY 1490 GACAAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1507  
DB 1590 GACAAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1607

## RESULT 15

US-11-376-990-3  
; Sequence 3, Application US/11376990  
; Publication No. US2006026997A1  
; GENERAL INFORMATION:  
; APPLICANT: Cunningham, Brian C.  
; APPLICANT: de Vos, Abraham M.  
; APPLICANT: Li, Bing  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR VARIANTS AND USES THEREOF  
; FILE REFERENCE: 11669.114USD1  
; CURRENT APPLICATION NUMBER: US/11/376,990  
; PRIOR FILING DATE: 2006-03-15  
; PRIOR APPLICATION NUMBER: US 09/546,857  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: US 60/184,235  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: US 60/129,788  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 990  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-376-990-3

Query Match 32.9%; Score 496.4; DB 7; Length 990;  
Best Local Similarity 99.8%; Pred. No. 3.2e-148;  
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1010 GCACCATGCGAGAGAGAGGAGGAGAAATCATCAGAAATGAGTGAATTCATGATGTC 1069  
DB 135 GCACCATGCGAGAGAGAGGAGGAGAAATCATCAGAAATGAGTGAATTCATGATGTC 194  
QY 1070 TATCAGCGGAGTACTGCTCCATTCAGATGAGACCTGTGTGACATCTTCCAGAGATACCTT 1129

DB 195 TATCAGCGGAGTACTGCTCCATTCAGATGAGACCTGTGTGACATCTTCCAGAGATACCTT 254  
QY 1130 GATGAGATGAGATGATCTTCAAGCCTGTGTGACATCTTCCAGAGATGAGTGTG 1189  
DB 255 GATGAGATGAGATGATCTTCAAGCCTGTGTGACATCTTCCAGAGATGAGTGTG 314  
QY 1190 TGCATGAGAGAGGAGGAGTGTGTGCTGAGAGATGAGATGAGATGAGATGAGATG 1249  
DB 315 TGCATGAGAGAGGAGGAGTGTGTGCTGAGAGATGAGATGAGATGAGATGAGATG 374  
QY 1250 ATGCGGATCAAACTTCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1309  
DB 375 ATGCGGATCAAACTTCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 434  
QY 1310 AAATGTGAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1369  
DB 435 AAATGTGAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 494  
QY 1370 TCAGAGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1429  
DB 495 TCAGAGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 554  
QY 1430 AACACAGACTGCGGTTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1489  
DB 555 AACACAGACTGCGGTTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 614  
QY 1490 GACAAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1507  
DB 615 GACAAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 632

Search completed: January 23, 2007, 04:01:15  
Job time : 1147 secs